

REMARKS

Claim Amendments

Claims 58-73 are currently pending in the application.

Claims 58 -61, 66-68 and 73 are newly amended and claims 76-79 are newly added.

These amendments and additions find support in the specification is discussed below.

Claims 62-65 and 69-72 which include methods directed to diagnosing moderate and marked osteoarthritis, have been cancelledled without prejudice or disclaimer, solely to expedite patent prosecution in accordance with the U.S. Patent Office Business Goals (65 Fed. Reg. 54604 (September 8, 2000)). Applicants reserve the right to present any cancelledled subject matter in a co-pending application.

Additionally, for the sole purpose of expediting prosecution in accordance with the U.S. Patent Office Business Goals (65 Fed. Reg. 54604 (September 8, 2000)), Applicant has amended the claims without prejudice or disclaimer, to include the limitations that the samples are obtained from cartilage, that the species being diagnosed is human, and that the genes comprising the claimed methods are the following ten elected genes: Beta 2 Microglobulin (B2M); Tumour Necrosis Factor Alpha-induced Protein (TNFAIP6); B-cell CLL/lymphoma 6 (zinc finger protein 51) (BCL6); Cyclin C (CCNC); Interleukin 13 receptor alpha 1 (IL13RA1); Bone Morphogenetic Protein 6 (BMP6); Calumenin (CALU); MAFB/Kreisler basic region/leucine zipper transcription factor (MAFB); Period 1 (PER1); Platelet Factor 4 (PF4); Calmodulin 1 (CALM1); Translationally Controlled Tumour Protein (TCTP). without prejudice or disclaimer, solely to expedite patent prosecution in accordance with the U.S. Patent Office Business Goals (65 Fed. Reg. 54604 (September 8, 2000)). Applicants reserve the right to present any cancelledled subject matter in a co-pending application.

Specifically support for the phrase “identifying markers of human osteoarthritis (OA)” is found throughout the specification, including: page 15 paragraph 209; page 21 paragraph 285; and page 27 Example 4;.

Support for the phrase “level of expression of RNA transcripts of a gene” is found throughout the specification, including: page 21, paragraph 285-286.

Support for the phrase “gene expression pattern” is found through the specification including: page 9 paragraph 139, and page 20 paragraph 275.

Support for the phrase “indicative of disease” is found throughout the specification, including: page 9 paragraph 138.

Claim Objections

Claims 58-73 are objected to because they refer to the Figures, and in particular Figure 6. As stated, incorporation by reference of a table is permitted in the exceptional circumstances where there is no practical way to define the invention in words, and where it is more concise to incorporate by reference rather than duplicating a drawing or table into the claim.

As per the restriction requirement, Applicant has amended the instant claims also to include the names of the 10 elected genes, and only refer to Figure 6 as illustrative of their differential expression in cartilage samples from normal and osteoarthritic humans.

In view of this amendment, Applicant respectfully requests reconsideration

Specification

It is suggested that Figures which contain text concerning the differential expression of genes in OA be converted into Tables so as to permit the information to be search accessible by the public. The Applicant will take this recommendation under consideration.

Drawings

As noted in the Office action, Figures 14 and 14A were removed by Applicant, the information therein being transferred to a sequence listing. In view of the removal of Figures 14 and 14A, the pages of the drawings have been renumbered, and the specification has been amended to delete references to Figures 14 and 14a. The specification has also been amended to reflect the renumbered figures including amendment of the brief description of the drawings section.

Compact Disc Submission

A replacement CD and identical copy thereof, with the sequence listing is submitted with this response. No new matter is added. This sequence listing is identical to now cancelledled Figure 14.

35 USC 112 Rejections

Indefiniteness

Claims 58-73 are rejected under 35 USC 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Examiner objects to the language “RNA transcripts which correspond to a gene” in claims 58-73 as being indefinite on the basis is not clear what RNA transcripts are meant to be encompassed by the claims. .”

However, claim terms are to be interpreted in light of the intrinsic evidence (*i.e.*, the claims at issue, the specification, and the prosecution history. See, *e.g.*, *McGill Inc. v. John Zink Co.*, 736 F.2d 666, 673-675, 221 U.S.P.Q. 944, 948-951 (Fed. Cir. 1984), *cert. denied*, 105 S.Ct. 514 (1984); *Fromson v. Advance Offset Plate, Inc.*, 720 F.2d 1565, 1569-1571, 219 U.S.P.Q. 1137, 1140-1141 (Fed. Cir. 1983)).

The specification describes the identification and sequence of numerous differentially expressed sequence tags (EST's) isolated from human cartilage which have been analyzed so as to identify the gene from which the ESTs were expressed (see for example, page 14 paragraph 196). The annotation process is described more fully on page 14 paragraph 194- page 15 paragraph 208 and teaches the mapping of the ESTs to the human genome using the Genbank/EMBL/DDBJ and dbEST database. Figure 6 discloses those human genes identified as a result of the disclosed process and provides a Genbank accession number of a species of RNA transcript expressed by the gene disclosed.

Moreover, claims should be construed as they would be by those skilled in the art. *Fromson*, 720 F.2d at 1571, 219 U.S.P.Q. at 1142. That is those skilled in the art would understand that “RNA transcripts which correspond to a gene” are those RNA transcripts which are transcribed from the gene. Nevertheless, Claims 58 and 60 have been amended to clarify that the RNA transcripts being claimed are those transcripts expressed from the genes identified in Table 6 as being differentially expressed in OA cartilage as compared with normal cartilage. Claims 59 and 61 further limit the selection of genes to those which are identified as being differentially expressed in OA cartilage as compared with normal cartilage and are further

selected from the following: Beta 2 Microglobulin (B2M); Tumour Necrosis Factor Alpha-induced Protein (TNFAIP6); B-cell CLL/lymphoma 6 (zinc finger protein 51) (BCL6); Cyclin C (CCNC); Interleukin 13 receptor alpha 1 (IL13RA1); Bone Morphogenetic Protein 6 (BMP6); Calumenin (CALU); MAFB/Kreisler basic region/leucine zipper transcription factor (MAFB); Period 1 (PER1); Platelet Factor 4 (PF4); Calmodulin 1 (CALM1); Translationally Controlled Tumour Protein (TCTP).

In view of the claim amendments and Applicant's arguments, reconsideration and withdrawal of the rejection is respectfully requested.

Enablement

Claims 58-73 are rejected under 35 USC 112, first paragraph, as failing to comply with the enablement requirement.

Examiner objects to claims 58-73 as failing to comply with the enablement requirement and in particular cites (a) the Nature of the Invention (b) the Scope of the Invention (c) the Guidance in the Specification and (d) the Teachings in the Prior Art and Level of Unpredictability and (e) Quantity of Experimentation. Applicant will address each of the points raised below.

Nature of the Invention

Examiner states that the claims recite a method of diagnosing osteoarthritis or a stage of OA which, as a result of the Examiner's Restriction Requirement, requires determining the level of the ten genes selected. Applicant respectfully disagrees. It is Applicant's understanding that because no prior art has been identified which identifies teaching any two of the selected ten genes as diagnostic of OA or a stage of OA, should the Applicant successfully overcome Examiner's objections and rejections, claims encompassing any two or more of the ten elected genes may be rejoined with the goal of allowance of these claims. Reconsideration of this issue is respectfully requested.

Examiner further indicates that the nature of the claimed invention requires knowledge that the genes are differentially expressed in OA or a stage of OA in such a way that one can reliably draw conclusions for the diagnosis of OA based on the gene expression patterns.

It is the Applicant's position that, the use of EST frequency to draw conclusions regarding differential expression is a scientifically acceptable technique (see for example Okubo *et al. Nature Genetics* 2, 173 - 179 (1992)), Kumar S, Connor JR, Dodds RA, Halsey W, Van Horn M, Mao J. *et al. Osteoarthritis Cartilage*. 2001 Oct;9(7):641-53; Dahl *et al. The Journal of Pathology* 2005 205 (1) 21-28.). Further evidence in support of this position is provided by way of an Inventor's Declaration wherein additional data obtained subsequent to filing of the Application is provided. In summary the data demonstrates that additional screening of the described cDNA libraries continues to support the biomarkers of Figure 6 as differentially expressed as between OA and non OA. In addition, using a second technique of either Affymetrix® microarray and/or ChondroChip™ microarray hybridization resulted in data which demonstrates the biomarkers of Figure 6 are differentially expressed as between OA and non OA. The analysis of the data is discussed more thoroughly in the section entitled "Guidance in the Specification and Working Examples".

Scope of the Invention

Examiner indicates that the scope of the language used in the claims is sufficiently broad to encompass (a) any sample including blood, synovial fluid and cartilage (b) all homologues, variants and the like and (c) all species of patient. In order to expedite examination, but without prejudice to the Applicant's rights to pursue related claims, Applicant has amended the claims so as to limit the claim to diagnosis of human osteoarthritis using cartilage samples. Applicant has clarified that the transcripts which are expressed from the gene identified are included within the scope of the claim. This would therefore include all transcripts which are expressed in cartilage from the gene of interest. This is consistent with the teaching within the specification wherein Applicant has identified numerous transcripts or portions thereof transcribed from the genes as shown in Figure 6.

Guidance in the Specification and Working Examples

Examiner argues that before reliable conclusions can be drawn regarding diagnosis or staging of OA, there are a number of issues that need to be addressed including those that follow:

(a) reliability of the EST frequency data to demonstrate differential gene expression (b) the lack of working examples of the claimed method for use in diagnosing of OA.

With regards to the former, as already mentioned, EST frequency data to draw conclusions regarding differential expression is a scientifically acceptable technique. The EST frequency analysis was done by analyzing and sequencing over 50,000 EST transcripts in a normal cartilage library, a mild OA cartilage library, and a severe OA cartilage library. Each of these ESTs was sequenced and matched to known genes where possible. As outlined in the Inventor's Declaration each of the cDNA libraries was constructed from two or more individuals and in particular the normal OA cartilage library was constructed using mRNA isolated from two individuals, the mild OA cartilage library was constructed using RNA isolated from six individuals, the severe OA cartilage library was constructed using RNA isolated from 3 individuals.

The decision in *In re Angstadt*, 190 U.S.P.Q. 218 (C.C.P.A. 1976) clearly states that every embodiment need not be disclosed, even in an unpredictable art, and clearly permits the presence of a screening step to identify those embodiments which possess the desired activity. In fact, in *Angstadt*, the Court specifically dismissed the notion that the specification must provide a level of guidance that would predict the outcome of an experiment (or reaction) "with reasonable certainty before performing the reaction" and that "such a proposition is contrary to the basic policy of the Patent Act, which is to encourage disclosure of inventions and thereby to promote progress in the useful arts."

Since filing of the patent application, Applicant has continued to identify ESTs from the four cDNA libraries following the methodologies as outlined in the specification. As can be seen in the Inventor's Declaration, in most cases where additional ESTs were identified, the EST frequency as between osteoarthritis libraries and normal libraries show the same trend (i.e. upregulated and or downregulated) when comparing osteoarthritis to non osteoarthritis as the original EST frequency data. This is true even in those cases where, as the Examiner notes, the number of ESTs identified originally is relatively few (see for example LAMC1; and IL13RA1). The Applicant also provides additional data obtained using microarray analysis of the selected genes to further support the utility of the biomarkers identified in Figure 6. Microarray analysis was performed using the methods as taught in the specification and hybridizing to either the

Affymetrix GeneChip® and/or the Applicant's own ChondroChip® constructed from some of the EST's identified. In particular RNA was isolated from the cartilage of numerous individuals having osteoarthritis and numerous individuals not having osteoarthritis and each RNA sample converted into cDNA for purposes of hybridization to the arrays. For most of the selected genes, the hybridization data is consistent with the EST frequency analysis and demonstrates statistical significant (i.e. a p value of less than 0.05) in differential expression as between individuals having osteoarthritis (where at least 7-10 individuals with osteoarthritis were used for the analysis of any one selected biomarker) and individuals not having osteoarthritis (where at least 10 individuals with osteoarthritis were used for the analysis of any one selected biomarker).

In three instances (B2M and ZFR, and TCTP) the data obtained by hybridization does not concord with the EST frequency data. As is understood, the law clearly does not require all of the species embodied within the scope of a claim to be operative for a claim to be valid (*Atlas Powder Co. v. E.I. du Pont de Nemours & Co.*, 750 F.2d 1569, 1577, 224 USPQ 409, 414 (Fed. Cir. 1984)). The microarray results still, however, in the case of B2M and ZFR demonstrate that the products of these genes are differentially expressed as between individuals having osteoarthritis and not having osteoarthritis.

Examiner further claims there is no guidance in the specification as to how the genes of the invention can be used for the diagnosis of OA. Applicant respectfully disagrees. The specification teaches the use of the genes of the invention for diagnosis of OA starting on page 21 paragraph 289-292. The specification further provides Example 9 as a working example of the invention in diagnosing OA. More specifically, the specification teaches isolation of an RNA sample from a test individual and hybridization of the RNA to a microarray comprised of nucleic acid members wherein at least one of the members corresponds to a gene which is identified as differentially expressed in individuals having osteoarthritis as compared to "normal" individuals (i.e. individuals not having osteoarthritis) to generate a gene expression pattern. As described in the definition of "indicative of disease" found on page 9, paragraph 133, an expression pattern is diagnostic if it is found significantly more often in patients with the disease than in patients without the disease using standards routine statistical methods. Thus the specification teaches how to use the genes of the invention for diagnosis of OA. The reconsideration and withdrawal of the rejection is respectfully requested.

Teachings in the Prior Art and Level of Unpredictability

Examiner further argues that is highly unpredictable whether the differential expression observed is due to OA or a stage of OA or if it represents a more generalized response to other conditions. With respect, Applicant disagrees. The genes of the invention were identified as those which are differentially expressed in the tissue at the site of the osteoarthritic decay, where it is known that the structural integrity of mature cartilage is in a delicate balance. Thus, it is expected that changes in the expression of the genes at this cartilage site are relevant to osteoarthritis and useful in its diagnosis. Furthermore, we identified many of the genes as being differentially expressed not only in the cartilage of osteoarthritic patients as compared with non osteoarthritic patients, but also as between different stages of osteoarthritis – again showing the likelihood that the differential expression of these genes is due to osteoarthritis.

As stated in the Manual of Patent Examining Procedure at 2164.03:

The “predictability or lack thereof” in the art refers to the ability of one skilled in the art to extrapolate the disclosed or known results to the claimed invention. If one skilled in the art can readily anticipate the effect of a change (in this case a change in gene expression in the cartilage of osteoarthritic patients as compared with non osteoarthritic patients) within the subject matter to which the claimed invention pertains, then there is predictability in the art.

As evidenced by Exhibit ”A” in the attached declaration, there is a high degree of correlation between the elected biomarker genes and their ability to monitor differential expression as between the cartilage of osteoarthritic patients as compared with the cartilage of non osteoarthritic patients. Absent evidence to the contrary, there is ample support for the conclusion that one skilled in the art would be able to extrapolate the results of the claimed invention including; (a) differential expression occurs in cartilage, (b) many of the genes identified are also differentially expressed as between different stages of osteoarthritis, (c) later correlating data obtained following the teachings as disclosed in the specification confirming the conclusion that the differential expression is indicative of osteoarthritis. Since the examiner has presented no evidence to the contrary, and one skilled in the art has the ability to anticipate the effect of the differential expression of the claimed genes to the claimed method of diagnosing osteoarthritis, predictability exists in the art.

Quantity of Experimentation

The Examiner suggests that the level of experimentation required to practice this invention are too enormous. In *In re Wands*, the court stated that “[e]nablement is not precluded by the necessity for some experimentation such as routine screening. However, experimentation needed to practice the invention must not be undue experimentation. ‘The key word is ‘undue’ not ‘experimentation’ (citing *In re Angstadt*, 537 F. 2d 498 at 504, 190 U.S.P.Q. 214 at 219 (C.C.P.A. 1976)). The Court also stated that “the test is not merely quantitative, since a considerable amount of experimentation is permissible, if it is merely routine, or if the specification in question provides a reasonable amount of guidance with respect to the direction in which the experimentation should proceed.” (citing *In re Jackson*, 217 U.S.P.Q. 804 at 807 (Bd. App. 1982)).

Applicant has already demonstrated that in their own work, they have been able to perform the experimentation necessary to determine that the genes elected are differentially expressed in normal patients as compared with those patients having osteoarthritis using microarray technology. This powerful technology allows one to test for expression of over 30,000 genes in one experiment for cartilage samples of numerous individuals, therefore Applicant has demonstrated that the experimentation necessary is not undue. In fact, all of the genes shown in Figure 6 can be analyzed in a single experiment for any individual. If the Examiner remains convinced that this is undue experimentation, Applicant would like information from the Examiner as to what is the quantity of experimentation that would not be considered undue experimentation and which would overcome the rejection.

Examiner further suggests that one would also have to show that the patterns of differential expression are specific to Osteoarthritis and not due to other diseases. Examiner indicates that in order to support a claim using these genes for diagnosis of OA, one would have to show that the genes are not differentially expressed in other disease areas. Applicant would point out that diagnosis, as is understood by a person skilled in the art, is not performed in the absence of other medical information including past history, symptoms, and the like. Therefore, it is not necessary that the biomarkers be tested to ensure that, for example, a person with a broken leg does not show the same pattern of differential expression. Diagnosis is often done in

combination with many other factors and tests. For example, commercially available tests for Rheumatoid Arthritis are routinely used despite the possibility of these tests indicating other possible conditions.

Reconsideration and withdrawal of the rejection is respectfully requested.

Conclusion

Applicant submits that all claims are allowable as written and respectfully request early favorable action by the Examiner. If the Examiner believes that a telephone conversation with Applicant's attorney/agent would expedite prosecution of this application, the Examiner is cordially invited to call the undersigned attorney/agent of record.

Respectfully submitted,

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Figure 14 - Relative EST Frequency of Unique Known Genes Common to Fetal and Normal cDNA Libraries - Page 1 of 17

Total ESTs from each library		13398	17151
Gene Name	Accession #	Fetal	Normal
1 alpha gene sequence (=HSP90)	AF203815.1	11 0.08%	561 3.27%
2 ribosomal DNA complete repeating unit	U13369.1	11 0.08%	303 1.77%
3 mitochondrial genome (consensus sequence)	X62996	112 0.84%	181 1.06%
4 decorin (DCN)	NM_001920.1	14 0.10%	172 1.00%
5 collagen type II alpha 1 (COL2A1)	J00116.1	172 1.28%	169 0.99%
6 osteonectin gene (SPARC) secreted protein, acidic, cysteine-rich	M25746.1	42 0.31%	149 0.87%
7 mitochondrion, complete genome (=AF382012.1 haplotype M*1 mitochondri	NC_001807.2	96 0.72%	141 0.82%
8 matrix Gla protein (MGP)	X53331	6 0.04%	140 0.82%
9 proteoglycan 4 (=megakaryocyte stimulating factor)	AAB09089.1	10 0.07%	138 0.80%
10 ribosomal protein S27 (=metallopainstimulin 1 MPS1)	NM_001030.1	38 0.27%	105 0.61%
11 putative p150	AAC51271.1	4 0.03%	99 0.58%
12 collagen type I alpha 2 (COL1A2)	NM_000089.1	153 1.14%	88 0.51%
13 beta-2 microglobulin gene (B2M)	gb AF072097.1	6 0.04%	88 0.51%
14 metallothionein 1L (MT1L)	NM_002450.1	2 0.01%	85 0.50%
15 connective tissue growth factor (CTGF)	U14750	6 0.04%	78 0.45%
16 collagen type III alpha 1 (COL3A1)	X06700	54 0.40%	77 0.45%
17 elongation factor 1 alpha 1 (EEF1A1)	NM_001402.1	150 1.12%	66 0.38%
18 scrapie responsive protein 1 (SCRG1)	NM_007281.1	3 0.02%	59 0.34%
19 tumor protein translationally-controlled 1 (TPT1)	NM_003295.1	45 0.34%	50 0.29%
20 fibronectin (FN)	X02761.1	16 0.12%	50 0.29%
21 ribosomal protein L41	AF026844.1	22 0.16%	47 0.27%
22 ribosomal RNA 18S	X03205	12 0.09%	47 0.27%
23 LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (=putative p150)	spP08547	1 0.01%	46 0.27%
24 reverse transCRiptase	D84391	1 0.01%	45 0.26%
25 ribosomal protein L7	X52967	45 0.34%	44 0.26%
26 fibromodulin (FMOD)	NM_002023.2	8 0.06%	41 0.24%
27 thymosin beta-4 (TMSB4X)	M17733	14 0.10%	40 0.23%
28 ribosomal protein S8 (RPS8)	NM_001012.1	42 0.31%	35 0.20%
29 ribosomal protein S6	M20020	27 0.20%	35 0.20%
30 ribosomal protein L21	U14967.1	17 0.13%	34 0.20%
31 lumican (LUM)	NM_002345.1	9 0.07%	33 0.19%
32 ubiquitin A-52 residue ribosomal protein fusion product 1 (UBA52)	gi4507760	7 0.05%	32 0.19%
33 vimentin gene (VIM)	Z19554	33 0.25%	31 0.18%
34 ribosomal protein S3a	M77234	22 0.16%	31 0.18%
35 ribosomal protein L31	NM_000993.1	15 0.11%	31 0.18%
36 ribosomal protein L9	U09953	47 0.35%	30 0.17%
37 annexin A2 (ANXA2)(lipocortin II)	NM_004039.1	14 0.10%	28 0.16%
38 ribonuclease, RNase A family, 1(pancreatic) (RefSeq aa 9e-73)	NP_002924.1	1 0.01%	28 0.16%
39 ribosomal protein L34 (RPL34)	NM_000995.1	23 0.17%	27 0.16%
40 Ribosomal protein L4	NM_000988.1	18 0.13%	27 0.16%
41 ribosomal protein L23	NM_000978.1	18 0.13%	27 0.16%
42 ribonuclease, RNase A	NM_002937.1	1 0.01%	27 0.16%
43 actin, beta (ACTB)	NM_001101.2	21 0.16%	25 0.15%
44 PRO2003	AF116679.1	14 0.10%	24 0.14%
45 ribosomal protein, large, P0 (RPLP0)	NM_001002.1	56 0.42%	23 0.13%
46 calmodulin 1 (phosphorylase kinase, delta) (CALM1)	NM_006888.1	7 0.05%	23 0.13%
47 collagen type I alpha 1 (COL1A1)	X06269	90 0.67%	22 0.13%
48 guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1 (G	NM_006098.1	21 0.16%	20 0.12%
49 SUI1 isolog	AF083441.1	8 0.06%	20 0.12%

MARKED UP COPY RENUMBERED FIGURES

Figure 10 - Relative EST Frequency of Unique Known Genes Common to Fetal and Normal cDNA Libraries - Page 2 of 17

50	NADH dehydrogenase	X81900	2	0.01%	20	0.12%
51	transcription elongation factor B (SIII), polypeptide 1-like (TCEB1L)	NM_003197.2	1	0.01%	20	0.12%
52	ribosomal protein S11 (RPS11)	NM_001015.1	38	0.28%	19	0.11%
53	ribosomal protein L37	L11567	34	0.25%	19	0.11%
54	H factor 1 (complement) (HF1)	NM_000186.1	1	0.01%	19	0.11%
55	collagen type XI alpha 1 (COL11A1)	NM_001854.1	46	0.34%	18	0.10%
56	ribosomal protein S4, X-linked (RPS4X)	NM_001007.1	33	0.25%	18	0.10%
57	S100 calcium-binding protein A4 (calcium protein, calvasculin, metastasin, gi4506764)	gi4506764	1	0.01%	18	0.10%
58	ribosomal protein L13a (RPL13A)	NM_012423.1	64	0.48%	17	0.10%
59	Ribosomal protein S20 (RPS20)	NM_001023.1	42	0.31%	17	0.10%
60	ribosomal protein L6	X69391	24	0.18%	17	0.10%
61	brain-expressed HHCPA78 homologue (VDUP1)	S73591	2	0.01%	17	0.10%
62	ribosomal protein L32 (RPL32)	NM_000994.1	38	0.28%	16	0.09%
63	ribosomal protein S29	L31610.1	18	0.13%	16	0.09%
64	transmembrane protein BRI	AF246221.1	4	0.03%	16	0.09%
65	cytochrome c oxidase subunit VIc (COX6C)	NM_004374.1	3	0.02%	16	0.09%
66	ribosomal protein L7a (surf 3) large subunit	M36072	25	0.19%	15	0.09%
67	signal recognition particle 14kD (homologous Alu RNA-binding protein)(SR)	NM_003134.1	3	0.02%	15	0.09%
68	ribosomal protein L30	L05095.1	24	0.18%	14	0.08%
69	translationally controlled tumor protein (TCTP)	X16064	23	0.17%	14	0.08%
70	TSC-22 protein	U35048	8	0.06%	14	0.08%
71	ribosomal protein L22 (RPL22)	NM_000983.1	6	0.04%	14	0.08%
72	nucleolar phosphoprotein B23 (NPM1)	M28699	4	0.03%	14	0.08%
73	clusterin (CLU) SP40.40 (=M63379 TRPM-2 protein)	NM_001831.1	1	0.01%	14	0.08%
74	RIBOSOMAL PROTEIN L10 (QM PROTEIN) (TUMOR SUPPRESSOR QM)	spP27635	53	0.40%	13	0.08%
75	ribosomal protein S12	X53505	35	0.26%	13	0.08%
76	ribosomal protein S25 (RPS25)	NM_001028.1	17	0.13%	13	0.08%
77	ribosomal protein S23 (RPS23) =D14530 (ORF)	NM_001025.1	8	0.06%	13	0.08%
78	thioredoxin (TXN)	J04026	4	0.03%	13	0.08%
79	SRY (sex-determining region Y)-box 9 (campomelic dysplasia, autosomal s	NM_000346.1	4	0.03%	13	0.08%
80	heat shock 10kD protein 1 (chaperonin 10) (HSP61)	NM_002167.1	1	0.01%	13	0.08%
81	ribosomal protein L37a	L22154	56	0.42%	12	0.07%
82	RIBOSOMAL PROTEIN L17	spP18621	31	0.23%	12	0.07%
83	ribosomal protein S17	M13932	28	0.21%	12	0.07%
84	ribosomal protein L27 (RPL27)	NM_000988.1	27	0.20%	12	0.07%
85	hH3.3B gene for histone H3.3	Z48950.1	10	0.07%	12	0.07%
86	ferritin L chain	M11147	9	0.07%	12	0.07%
87	ribosomal protein L24 (RPL24) (=ribosomal protein L30)	NM_000986.1	8	0.06%	12	0.07%
88	lysosomal membrane glycoprotein CD63 (=M59907 ME491;X07982)	M58485	7	0.05%	12	0.07%
89	CD63 antigen (melanoma 1 antigen) (CD63)	NM_001780.1	7	0.05%	12	0.07%
90	histone H3.3	Z48950	3	0.02%	12	0.07%
91	t-complex-associated-testis-expressed 1-like 1 (TCTEL1)	NM_006518.1	2	0.01%	12	0.07%
92	procollagen C-endopeptidase enhancer 2 (PCOLCE2)	NM_013363.1	1	0.01%	12	0.07%
93	electron transfer flavoprotein alpha-subunit	J04058.1	1	0.01%	12	0.07%
94	Ribosomal protein L36 (=RPL44)	AF077043.1	20	0.15%	11	0.06%
95	ribosomal protein L39	D79205	15	0.11%	11	0.06%
96	MORF-related gene X (KIAA0026) (=MRG15)	NM_012286.1	2	0.01%	11	0.06%
97	PRO1574 (mitochondrial proteolipid 68MP homolog (PLPM)	AF116639.1	2	0.01%	11	0.06%
98	reverse transcriptase related protein	prf1207289A	1	0.01%	11	0.06%
99	ribosomal protein L3 (RPL3)	NM_000967.1	42	0.31%	10	0.06%
100	ribosomal protein L13	AF112214	33	0.25%	10	0.06%
101	actin, gamma 1 (ACTG1)	NM_001614.1	31	0.23%	10	0.06%

MARKED UP COPY RENUMBERED FIGURES

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Figure 15 - Relative EST Frequency of Unique Known Genes Common to Fetal and Normal cDNA Libraries - Page 3 of 17

102	RIBOSOMAL PROTEIN L10A (CSA-19)(RPL10A)	P53025	18	0.13%	10	0.06%
103	ribosomal protein L35a	NM_000996.1	14	0.10%	10	0.06%
104	eukaryotic translation Initiation factor 3 (EIF3S6) (=INT6)	NM_001568.1	13	0.10%	10	0.06%
105	H2A histone family, member Z (H2AFZ) = D28450.1	NM_002108.1	4	0.03%	10	0.06%
106	zinc finger protein 218 (ZNF218)	AF062072.1	3	0.02%	10	0.06%
107	cytochrome c oxidase subunit II gene (ORF)	AF004339	3	0.02%	10	0.06%
108	TPT1 gene for translationally controlled tumor protein (TCTP), exons 1-6	AJ400717.1	2	0.01%	10	0.06%
109	selenoprotein P (SEPP1)	Z11783	1	0.01%	10	0.06%
110	ribosomal protein S15a	X84407	23	0.17%	9	0.05%
111	cytoskeletal gamma-actin	X04098	19	0.14%	9	0.05%
112	prothymosin alpha	M14630	18	0.13%	9	0.05%
113	ribosomal protein S13	NM_001017.1	17	0.13%	9	0.05%
114	ATP synthase, H transporting, mitochondrial F0 complex, subunit g (ATP5H)	Hs.107476	4	0.03%	9	0.05%
115	defender against cell death 1 (DAD1)	NM_001344.1	3	0.02%	9	0.05%
116	TI-227H (=tomoregulin; mitochondrial)	D50625	2	0.01%	9	0.05%
117	ATPase, H transporting, lysosomal (vacuolar proton pump) 9kD (ATP9H)	NM_003945.1	1	0.01%	9	0.05%
118	nuclear pore complex interacting protein (NPIC)	AF132984.1	1	0.01%	9	0.05%
119	ribosomal protein S24	M31520	23	0.17%	8	0.05%
120	ribosomal protein L5	U76609	23	0.17%	8	0.05%
121	heterogeneous nuclear ribonucleoprotein A1 (HNRPA1)	NM_002136.1	14	0.10%	8	0.05%
122	polyubiquitin	E12605	13	0.10%	8	0.05%
123	ribosomal protein L12	L06505	12	0.09%	8	0.05%
124	ribosomal protein L38	Z26876	8	0.06%	8	0.05%
125	poly(A)-binding protein (PABP)	U68105	6	0.04%	8	0.05%
126	carboxypeptidase E (CPE)	NM_001873.1	6	0.04%	8	0.05%
127	cytochrome b (ORF)	U09500	5	0.04%	8	0.05%
128	Tigger1 transposable element	U49973.1	5	0.04%	8	0.05%
129	NADH dehydrogenase(ubiquinone) Fe-S protein 5 (15kD) (NADH-coenzyme F5)	NM_004552.1	4	0.03%	8	0.05%
130	thrombospondin 4 (THBS4)	NM_003248.1	4	0.03%	8	0.05%
131	F1-ATPase epsilon-subunit (ATP5E)	AF052955.1	3	0.02%	8	0.05%
132	frizzled-related protein (FRZB)	NM_001463.1	3	0.02%	8	0.05%
133	glucocorticoid-induced GILZ	AF228339	3	0.02%	8	0.05%
134	Fritz mRNA, complete cds	U91803.1	2	0.01%	8	0.05%
135	actin, alpha, cardiac muscle	NP_005150.1	2	0.01%	8	0.05%
136	vacuolar H-ATPase subunit	AF038954	1	0.01%	8	0.05%
137	serine/threonine protein kinase Kp78 splice variant CTAK75a	AF159295.1	1	0.01%	8	0.05%
138	ribosomal protein L27A	AB020236.1	34	0.25%	7	0.04%
139	ribosomal protein, large P2 (RPLP2)	NM_001004.1	14	0.10%	7	0.04%
140	tumor rejection antigen (gp96) 1 (TRA1)	X15187	10	0.07%	7	0.04%
141	ribosomal protein S7	M77233	8	0.06%	7	0.04%
142	guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 1 (G12)	BC008855.1	8	0.06%	7	0.04%
143	matrilin-3 (MATR3)	Y13341	7	0.05%	7	0.04%
144	guanine nucleotide binding protein (G protein), alpha stimulating activity polypeptide 2 (G13)	NM_000516.2	7	0.05%	7	0.04%
145	lysosome-associated protein, transmembrane - 4alpha (=D14696.1 Human)	U34259.1	6	0.04%	7	0.04%
146	Cyr61 protein (CYR61)	AF031385	6	0.04%	7	0.04%
147	ribosomal protein S26	NM_001029.1	6	0.04%	7	0.04%
148	serine protease=HTRA serine protease (PRSS11)=AF157623.1	Y07921	5	0.04%	7	0.04%
149	hexabrachion (tenascin C, cytactin) (HXB)	NM_002160.1	4	0.03%	7	0.04%
150	palladin (KIAA0992)= CGI-151	NM_016081.1	3	0.02%	7	0.04%
151	collagen lysyl hydroxylase isoform 2 (PLOD2)	U84573	2	0.01%	7	0.04%
152	myosin, light polypeptide, regulatory, non-sarcomeric (20kD) (MLCB), mRNA	Hs.233936	2	0.01%	7	0.04%
153	procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2 (PLOD1)	Hs.41270	2	0.01%	7	0.04%

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154	KVLQT1 gene (=p150)	AJ006345.1	2	0.01%	7	0.04%
155	suppression of tumorigenicity 13 (Hsp70-interacting protein) (ST13)	NM_003932.1	2	0.01%	7	0.04%
156	spermidine/spermine N1-acetyltransferase	Z14136	1	0.01%	7	0.04%
157	epithelial membrane protein 1 (EMP1)	NM_001423.1	1	0.01%	7	0.04%
158	muscleblind (Drosophila)-like (MBNL) (=KIAA0428)	NM_021038.1	1	0.01%	7	0.04%
159	SOD-2 manganese superoxide dismutase	X65965	1	0.01%	7	0.04%
160	heat shock 70kD protein 10 (HSC71) (HSPA10)	NM_006597.1	1	0.01%	7	0.04%
161	MADSMEF2-family transcription factor (MEF2C) mRNA, complete cds	L08895.1	1	0.01%	7	0.04%
162	ribosomal protein L15	NM_002948.1	26	0.19%	6	0.03%
163	collagen type IX alpha 3 (COL9A3)	AF026802.1	26	0.19%	6	0.03%
164	ribosomal protein L26	X69392	18	0.13%	6	0.03%
165	FK506 binding protein (Fkbp63)	AF090334	8	0.06%	6	0.03%
166	nascent polypeptide-associated complex alpha polypeptide (NACA)	NM_005594.1	6	0.04%	6	0.03%
167	collagen type XIV variant C-terminal NC1 and 3'UTR	Y11711	6	0.04%	6	0.03%
168	Tis11d gene	U07802	5	0.04%	6	0.03%
169	transforming growth factor beta-stimulated protein TSC-22 (TSC22)	NM_006022.1	5	0.04%	6	0.03%
170	ADP/ATP translocase	J03592	5	0.04%	6	0.03%
171	ferritin heavy chain	L20941.1	4	0.03%	6	0.03%
172	testis enhanced gene transCRipt protein (TEGT)	AF033095	4	0.03%	6	0.03%
173	translocation protein 1(TLOC1)	NM_003262.1	3	0.02%	6	0.03%
174	mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjugating	AF224669.1	3	0.02%	6	0.03%
175	lactate dehydrogenase B (LDH-B)	Y00711	3	0.02%	6	0.03%
176	peroxiredoxin 1 (PRDX1) (=NKEFA)	NM_002574.1	3	0.02%	6	0.03%
177	membrane protein CH1 (CH1)	AB020980	3	0.02%	6	0.03%
178	fibroblast activation protein, alpha; seprase (FAP)	NM_004460.1	2	0.01%	6	0.03%
179	cig19 (=D31887.1 KIAA0062)	AF026940.1	1	0.01%	6	0.03%
180	transmembrane protein (CD59)	M84349.1	1	0.01%	6	0.03%
181	chloride intracellular channel 4 like (CLIC4L)	NM_013943.1	1	0.01%	6	0.03%
182	protein C inhibitor [human, leukocytes, Genomic, 1402 nt, segment 5 of 5]	S69366.1	1	0.01%	6	0.03%
183	ubiquitin-conjugating enzyme E2B (RAD6 homolog) (UBE2B)	NM_003337.1	1	0.01%	6	0.03%
184	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1(NFKB)	AF213884.1	1	0.01%	6	0.03%
185	tubulin beta	AF070561	19	0.14%	5	0.03%
186	ribosomal protein L44 (RPL44)	NM_001001.1	14	0.10%	5	0.03%
187	v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS)	NM_005252.2	12	0.09%	5	0.03%
188	triosephosphate isomerase (TPI1)	M10036	8	0.06%	5	0.03%
189	myosin regulatory light chain	X54304	6	0.04%	5	0.03%
190	lysyl oxidase	U22384	6	0.04%	5	0.03%
191	insulin-like growth factor binding protein 5 (IGFBP5) gene	L27556.1	6	0.04%	5	0.03%
192	cathepsin K (pseudosclerosis)(CTSK)	NM_000396.1	5	0.04%	5	0.03%
193	B-cell translocation protein 1 (BTG1)	X61123	5	0.04%	5	0.03%
194	cytochrome c oxidase subunit VIIb	Z14244	4	0.03%	5	0.03%
195	cell division cycle 10 (homologous to CDC10 of S. cerevisiae) (CDC10)	NM_001788.1	4	0.03%	5	0.03%
196	activating transCRiption factor 4 (tax-responsive enhancer element B67) (Agi4502264)		4	0.03%	5	0.03%
197	integral membrane protein 2A (ITM2A)	NM_004867.1	4	0.03%	5	0.03%
198	transforming growth factor beta-induced, 68kD (TGFB1)	NM_000358.1	3	0.02%	5	0.03%
199	eukaryotic translation initiation factor 4 gamma, 2 (EIF4G2)	NM_001418.1	3	0.02%	5	0.03%
200	Sec61 gamma	AF054184	3	0.02%	5	0.03%
201	mitochondrial signal peptidase	AF061737	3	0.02%	5	0.03%
202	actin binding protein ABP620	AB029290.1	3	0.02%	5	0.03%
203	WSB-1 isoform	AF106884.1	3	0.02%	5	0.03%
204	heterogeneous nuclear ribonucleoprotein A2/B1 (HNRPA2B1)	NM_002137.1	3	0.02%	5	0.03%
205	peptidylglycine alpha-amidating monooxygenase (PAM)	M37721	2	0.01%	5	0.03%

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Figure 14 - Relative EST Frequency of Unique Known Genes Common to Fetal and Normal cDNA Libraries - Page 5 of 17

206	small nuclear ribonucleoprotein D2 polypeptide (16.5kD) (SNRPD2)	NM_004597.3	2	0.01%	5	0.03%
207	syndecan binding protein (syntenin) (SDCBP)(ORF) = AF000652.1	NM_005625.1	2	0.01%	5	0.03%
208	JKTBP2, JKTBP1, complete cds	AB017018.1	2	0.01%	5	0.03%
209	cartilage intermediate layer protein, CILP	AB022430.1	1	0.01%	5	0.03%
210	ring-box 1 (RBX1)	NM_014248.1	1	0.01%	5	0.03%
211	allograft inflammatory factor 1 (AIF1)	NM_001623.2	1	0.01%	5	0.03%
212	fragile 16D oxidoreductase (FOR)	AF217490.1	1	0.01%	5	0.03%
213	PRO1873	AF119859.1	1	0.01%	5	0.03%
214	poly(rC)-binding protein 2 (PCBP2)	NM_005016.1	1	0.01%	5	0.03%
215	collagen type IX alpha 1 (COL9A1)(ORF)	NM_001851.1	74	0.55%	4	0.02%
216	collagen type XI alpha2 (COL11A2)	U41068.1	34	0.25%	4	0.02%
217	lectin, galactoside-binding, soluble, 1 (galectin 1) (LGALS1)mRNA (=14 kd)	NM_002305.2	22	0.16%	4	0.02%
218	T-cell cyclophilin	Y00052	18	0.13%	4	0.02%
219	chondromodulin 1 precursor (CHM-1)	NM_007015.1	15	0.11%	4	0.02%
220	ribosomal protein L14	D87735	12	0.09%	4	0.02%
221	heparan sulfate proteoglycan (HSPG) (OCI5)	J04621.1	9	0.07%	4	0.02%
222	annexin A5 (ANXA5)(lipocortin-V)	NM_001154.2	9	0.07%	4	0.02%
223	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member	NM_005888.1	6	0.04%	4	0.02%
224	nuclear protein SDK3 (=MEMA)	Y10351	6	0.04%	4	0.02%
225	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4 (9kD, MLRQ) (NM_002489.1)	NM_002489.1	5	0.04%	4	0.02%
226	collagen type VI alpha 3 (COL6A3)	NM_004369.1	5	0.04%	4	0.02%
227	enhancer of rudimentary homologue	U66871	5	0.04%	4	0.02%
228	HSPC330 mRNA(=HSPC016)	AF161448.1	5	0.04%	4	0.02%
229	peripheral myelin protein 22	M94048	5	0.04%	4	0.02%
230	bone sialoprotein (BNSP)	L10363.1	5	0.04%	4	0.02%
231	lactate dehydrogenase A (LDHA)	NM_005588.1	4	0.03%	4	0.02%
232	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein	NM_003404.1	4	0.03%	4	0.02%
233	heterogeneous nuclear ribonucleoprotein D-like (HNRPL)	NM_005463.1	4	0.03%	4	0.02%
234	heterogeneous nuclear ribonucleoprotein D (hnRNP D) (52% aa)	D55671	4	0.03%	4	0.02%
235	platelet-derived growth factor receptor alpha (PDGFRA)	M21574	4	0.03%	4	0.02%
236	cyclin I	D50310	4	0.03%	4	0.02%
237	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform (PPP2	NM_002715.1	4	0.03%	4	0.02%
238	melanoma growth regulatory protein MIA	X75450	4	0.03%	4	0.02%
239	phosphoglycerate kinase 1 (PGK1) (ORF)	NM_000291.1	3	0.02%	4	0.02%
240	Heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	NM_004501.1	3	0.02%	4	0.02%
241	alpha-2-macroglobulin	D83196	3	0.02%	4	0.02%
242	sin3 associated polypeptide (SAP18)	AF153608	3	0.02%	4	0.02%
243	ubiquinol-cytochrome c reductase complex (7.2 kD); hypothetical protein	RNP_037519.1	2	0.01%	4	0.02%
244	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5 (RNA helicase, 68kD) (D	NM_004398.1	2	0.01%	4	0.02%
245	GAP-associated tyrosine phosphoprotein p62 (Sam68) (SAM68) (=p62)	NM_006559.1	2	0.01%	4	0.02%
246	latent transforming growth factor beta binding protein 1 (LTBP1)	NM_000627.1	2	0.01%	4	0.02%
247	myosin, light polypeptide 1, alkali; skeletal, fast (MYL1)	NM_002475.1	2	0.01%	4	0.02%
248	melanoma inhibitory	NM_006533.1	2	0.01%	4	0.02%
249	integrin beta 1 subunit	X07979.1	1	0.01%	4	0.02%
250	TGF-beta1R alpha	D50683	1	0.01%	4	0.02%
251	CGI-110 protein	AF151868.1	1	0.01%	4	0.02%
252	HS1 protein (=YWHAQ)	X57347	1	0.01%	4	0.02%
253	cytochrome c oxidase subunit VIIa polypeptide 2 like (COX7A2L)	NM_004718.1	1	0.01%	4	0.02%
254	zinc finger transcription factor GKLF	AF105036.1	1	0.01%	4	0.02%
255	KIAA0438	AB007898.1	1	0.01%	4	0.02%
256	T245 protein (T245) =TM4SF8=TM4-D	AF043906	1	0.01%	4	0.02%
257	SMT3 (suppressor of mif two 3, yeast) homolog 2 (SMT3H2)	NM_006937.1	1	0.01%	4	0.02%

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258	AD-017 protein	AF157318.1	1	0.01%	4	0.02%
259	KIAA0164	D79888	1	0.01%	4	0.02%
260	laminin B2 chain	M55210	1	0.01%	4	0.02%
261	TRAM protein	CAA45218.1	1	0.01%	4	0.02%
262	dual specificity phosphatase 1 (DUSP1)	NM_004417.2	1	0.01%	4	0.02%
263	over-expressed breast tumor protein	L34839	1	0.01%	4	0.02%
264	cathepsin L (CTSL)	NM_001912.1	1	0.01%	4	0.02%
265	chondroitin sulfate proteoglycan 2 (versican) (CSPG2)	NM_004385.1	1	0.01%	4	0.02%
266	ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1)	NM_003349.1	1	0.01%	4	0.02%
267	integrin alpha 10 subunit (ITGA10)	AF112345.1	1	0.01%	4	0.02%
268	signal sequence receptor, gamma (translocon-associated protein gamma)	NM_007107.1	1	0.01%	4	0.02%
269	fragile X mental retardation 1 (FMR1)	NM_002024.1	1	0.01%	4	0.02%
270	X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and	AF003528.1	1	0.01%	4	0.02%
271	secreted frizzled-related protein 1 (SFRP1)	NM_003012.2	1	0.01%	4	0.02%
272	proteasome (prosome macropain) beta type, 4 (PSMB4)	NM_002796.1	1	0.01%	4	0.02%
273	thrombospondin 3 (THBS3) (RefSeq aa 3e-59)	NP_009043.1	1	0.01%	4	0.02%
274	laminin, gamma 1 (formerly LAMB2) (LAMC1)	NM_002293.2	1	0.01%	4	0.02%
275	ribosomal protein S21 (RPS21)	L04483	21	0.16%	3	0.02%
276	ribosomal protein L19	X63527	16	0.12%	3	0.02%
277	Tubulin alpha isoform 1	AF081484	16	0.12%	3	0.02%
278	H3 histone, family 3A (H3F3A)	NM_002107.1	8	0.06%	3	0.02%
279	ribophorin II (RPN2)	Y00282	7	0.05%	3	0.02%
280	neural precursor cell expressed, developmentally down-regulated 5 (NEDD)	NM_004404.1	6	0.04%	3	0.02%
281	heat shock 90kD protein 1 beta (HSPCB)	NM_007355.1	6	0.04%	3	0.02%
282	eukaryotic translation elongation factor 1 gamma (EEF1G)	NM_001404.1	6	0.04%	3	0.02%
283	dynein light chain 1 (hdc1), cytoplasmic	U32944	5	0.04%	3	0.02%
284	GABA(A) receptor-associated protein (GABARAP)	NM_007278.1	5	0.04%	3	0.02%
285	cyclophilin B (hCyPB)	M60857	5	0.04%	3	0.02%
286	cytochrome c oxidase, liver specific (EC 1.9.3.1.)	X15822	4	0.03%	3	0.02%
287	mitochondrial ubiquinone-binding protein	M26700	4	0.03%	3	0.02%
288	low molecular mass ubiquinone-binding protein	D50369	4	0.03%	3	0.02%
289	protein tyrosine phosphatase (hR-PTP)	X58288	4	0.03%	3	0.02%
290	Huntingtin Interacting protein	AF049103	4	0.03%	3	0.02%
291	interCRine-alpha (hIRH)	U19495	4	0.03%	3	0.02%
292	cathepsin B (CTSB)	L22569	3	0.02%	3	0.02%
293	thyroid receptor interactor (TRIP7)	L40357	3	0.02%	3	0.02%
294	pre-mRNA splicing factor (SFRS3)	AF107405.1	3	0.02%	3	0.02%
295	alpha E-catenin (CTNNA1) gene	AF102803.1	3	0.02%	3	0.02%
296	profilin II	L10678.1	3	0.02%	3	0.02%
297	16.7Kd protein	AF078845.1	3	0.02%	3	0.02%
298	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein	NM_006826.1	3	0.02%	3	0.02%
299	prostatic binding protein (PBP)	NM_002567.1	3	0.02%	3	0.02%
300	nidogen-2	AJ223500	3	0.02%	3	0.02%
301	valosin-containing protein(VCP)	NM_007126.2	3	0.02%	3	0.02%
302	tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinf)	NM_000382.1	2	0.01%	3	0.02%
303	cytochrome c oxidase subunit VIc (COX7C)	NM_001867.1	2	0.01%	3	0.02%
304	ubiquitin-like 1 (sentrin) (UBL1) (=SUMO-1)	NM_003352.1	2	0.01%	3	0.02%
305	cytosolic selenium-dependent glutathione peroxidase (=L09159 RHOA prot	M83094	2	0.01%	3	0.02%
306	BCL2/adenovirus E1B 19kD-interacting protein 3 (BNIP3)	U15174	2	0.01%	3	0.02%
307	NADH dehydrogenase subunit 2 (ND2)	AF014897.2	2	0.01%	3	0.02%
308	poly(A)-binding protein, cytoplasmic 1 (PABPC1)	NM_002568.1	2	0.01%	3	0.02%
309	PAPS synthetase-2 (PAPSS2)	AF074331.1	2	0.01%	3	0.02%

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Figure 14 Relative EST Frequency of Unique Known Genes Common to Fetal and Normal cDNA Libraries - Page 7 of 17

310	TATA box binding protein (TBP)-associated factor, RNA polymerase II, F, 5	NM_005642.1	2	0.01%	3	0.02%
311	MAGUK protein p57 (=AB002323 KIAA0325)	AF162130.1	2	0.01%	3	0.02%
312	adaptor-related protein complex 3, sigma 1 subunit (CLAPS3)	NM_001284.1	2	0.01%	3	0.02%
313	KIAA0372	AB002370.1	2	0.01%	3	0.02%
314	ubiquinol-cytochrome c reductase hinge protein (UQCRH)	NM_006004.1	2	0.01%	3	0.02%
315	non-histone chromosome protein 2 (S. cerevisiae)-like 1 (NHP2L1)=D5042	NM_005008.1	2	0.01%	3	0.02%
316	heterogeneous nuclear ribonucleoprotein M (HNRPM)	5174610	2	0.01%	3	0.02%
317	Golgi apparatus protein 1 (GLG1)	NM_012201.1	2	0.01%	3	0.02%
318	moesin (MSN)	NM_002444.1	2	0.01%	3	0.02%
319	nucleolar phosphoprotein p130 (P130)	NM_004741.1	2	0.01%	3	0.02%
320	neuroendocrine-specific protein C like (foocan) (NSP-CL) reticulon 4 (RTN)	NM_007008.1	1	0.01%	3	0.02%
321	mitochondrial proteolipid 68MP homolog (PLPM)	NM_004894.1	1	0.01%	3	0.02%
322	hepatitis B virus X interacting protein (XIP)	AF029890	1	0.01%	3	0.02%
323	activated RNA polymerase (PC4)	NM_006713.1	1	0.01%	3	0.02%
324	FRG1	L76159	1	0.01%	3	0.02%
325	CD164 antigen, sialomucin (CD164)	NM_006016.1	1	0.01%	3	0.02%
326	ganglioside expression factor 2 (GEF-2)	NM_007285.1	1	0.01%	3	0.02%
327	S164 (=AC004858 U1 small ribonucleoprotein 1SNRP homologue)	AF109907	1	0.01%	3	0.02%
328	sema domain immunoglobulin domain (Ig)(semaphorin) 3E (SEMA3E)(= K1	NM_012431.1	1	0.01%	3	0.02%
329	prion protein (p27-30) (Creutzfeld-Jakob disease, Gerstmann-Straussler-Sch	NM_000311.1	1	0.01%	3	0.02%
330	interleukin 1 receptor, type I (IL1R1) = M27492.1	NM_000877.1	1	0.01%	3	0.02%
331	zinc finger protein 9 (a cellular retroviral nucleic acid binding protein)	(g)4827070	1	0.01%	3	0.02%
332	KIAA0242	D87684	1	0.01%	3	0.02%
333	PPP1R5	AF110824.1	1	0.01%	3	0.02%
334	transforming, acidic coiled-coil containing protein 1 (TACC1=AF049910	NM_006283.1	1	0.01%	3	0.02%
335	clathrin, light polypeptide (Lca) (CLTA)	NM_007096.1	1	0.01%	3	0.02%
336	KIAA0069 gene	D31885.1	1	0.01%	3	0.02%
337	uncharacterized bone marrow protein BM034 (=AK000571 FLJ20564 fis) (=	AF217511.1	1	0.01%	3	0.02%
338	Membrane cofactor protein	X59408.1	1	0.01%	3	0.02%
339	KIAA0349 gene	AB002347.1	1	0.01%	3	0.02%
340	TGF-beta inducible early protein (TIEG)	U21847	1	0.01%	3	0.02%
341	CD59 antigen p18-20 (antigen identified by monoclonal antibodies 16.3A5,	NM_000611.1	1	0.01%	3	0.02%
342	signal peptidase complex (18kD) (SPC18)	NM_014300.1	1	0.01%	3	0.02%
343	archain 1 (ARCN1)	g4502194	1	0.01%	3	0.02%
344	selenoprotein W (hSelW)	AF015283.1	1	0.01%	3	0.02%
345	nuclear factor I/B (NFIB)	NM_005596.1	1	0.01%	3	0.02%
346	KIAA0174	D79996	1	0.01%	3	0.02%
347	heterogeneous nuclear ribonucleoprotein H1 (H) (HNRPH1)	NM_005520.1	1	0.01%	3	0.02%
348	calcium modulating cyclophilin ligand CAMLG (CAMLG)	AF068179.1	1	0.01%	3	0.02%
349	KIAA0527	AB011099.1	1	0.01%	3	0.02%
350	retrovirus-related hypothetical protein II (=X52235 ORFII)	S23650	1	0.01%	3	0.02%
351	polymerase (RNA) II polypeptide G (POLR2G)	NM_002696.1	1	0.01%	3	0.02%
352	peptidylprolyl isomerase A (cyclophilin A) (PPIA), mRNA /cds=(44,541) /gb	Hs.342389	1	0.01%	3	0.02%
353	S100 calcium-binding protein, beta (neural) (S100B)	NM_006272.1	1	0.01%	3	0.02%
354	phosphatidic acid phosphatase 2b (PPAP2B)	AB000889	1	0.01%	3	0.02%
355	KIAA1354	AB037775	1	0.01%	3	0.02%
356	glycyl-tRNA synthetase; glycine tRNA ligase (RefSeq aa 1e-45)	NP_002038.1	1	0.01%	3	0.02%
357	coagulation factor XIII, A1 polypeptide (F13A1)	NM_000129.1	1	0.01%	3	0.02%
358	CGI-31 protein (LOC51075)	NM_015959.1	1	0.01%	3	0.02%
359	caltractin (20kD calcium-binding protein) (CALT)	NM_004344.1	1	0.01%	3	0.02%
360	PC3 cell line (TL27)	X75684.1	1	0.01%	3	0.02%
361	glyceraldehyde 3-phosphate dehydrogenase (GADPH)	J02642	41	0.31%	2	0.01%

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Figure 16 - Relative EST Frequency of Unique Known Genes Common to Fetal and Normal cDNA Libraries - Page 8 of 17

362	ribosomal protein S5 (RPS5)	NM_001009.1	29	0.22%	2	0.01%
363	ribosomal protein L35	U12465	27	0.20%	2	0.01%
364	ribosomal protein S3 (RPS3)	NM_001005.1	21	0.16%	2	0.01%
365	cartilage link protein (CRTL1)	U43328.1	20	0.15%	2	0.01%
368	ribosomal protein S16	M60854	14	0.10%	2	0.01%
367	laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1)(ORF)	NM_002295.1	12	0.09%	2	0.01%
368	ribosomal protein L23a	U43701	11	0.08%	2	0.01%
369	ribosomal protein S15 (RPS15) (=insulinoma rig-analog encoding DNA-bind	NM_001018.1	11	0.08%	2	0.01%
370	elongation factor 1 beta 2 (EEF1B2)	NM_001959.1	10	0.07%	2	0.01%
371	collagenase type IV	J03210	10	0.07%	2	0.01%
372	RNA polymerase II elongation factor-like protein	Z47087	8	0.06%	2	0.01%
373	calumenin (Calu) (calumenin)	AF013759	8	0.06%	2	0.01%
374	calreticulin (CALR)	M84739	7	0.05%	2	0.01%
375	1-8U gene from interferon-inducible gene family	X57352.1	6	0.04%	2	0.01%
376	BIP protein	X87949	5	0.04%	2	0.01%
377	ATP synthase, H transporting, mitochondrial F1 complex, gamma polypep	NM_005174.1	5	0.04%	2	0.01%
378	ATP synthase, H transporting, mitochondrial F1 complex, alpha subunit, ls	NM_004046.1	5	0.04%	2	0.01%
379	thrombospondin 2 (THBS2)	L12350	5	0.04%	2	0.01%
380	thrombospondin 1 (THBS1)	NM_003246.1	5	0.04%	2	0.01%
381	cytosolic thyroid hormone-binding protein (=M23725 M2-type pyruvate kina	M26252	5	0.04%	2	0.01%
382	fatty acid binding protein (adipocyte lipid-binding protein)	NM_001442.1	4	0.03%	2	0.01%
383	78 kD glucose-regulated protein (GRP78) gene (=BIP protein)	M19645.1	4	0.03%	2	0.01%
384	fibrillin (FBN1)	X63556	4	0.03%	2	0.01%
385	nuclease sensitive element binding protein 1 (NSEP1) = L28809.1 dbpB-lik	NM_004559.1	4	0.03%	2	0.01%
386	HSPC016, mRNA /cds=(38,232) /gb=Nm_015933 /gi=7705430 /ug=Hs.171	Hs.171774	4	0.03%	2	0.01%
387	cellular growth-regulating protein	L10844	4	0.03%	2	0.01%
388	anti-oxidant protein 2 (non-selenium glutathione peroxidase, acidic calcium	NM_004905.1	4	0.03%	2	0.01%
389	small EDRK-rich factor 2 (SERF2)	NM_005770.1	4	0.03%	2	0.01%
390	chondroadherin (CHAD)	U96769	4	0.03%	2	0.01%
391	general transcription factor 2-I (GTF2I)	AF038968	4	0.03%	2	0.01%
392	CD9 antigen (p24/CD9)	L08125	3	0.02%	2	0.01%
393	prefoldin 5 (PFDN5) (=D89667 c-myc binding protein)	NP_002615.1	3	0.02%	2	0.01%
394	tomoregulin	AB004064.1	3	0.02%	2	0.01%
395	phenylalkylamine binding protein gene	AF196969.1	3	0.02%	2	0.01%
396	ERF-1	X79067.1	3	0.02%	2	0.01%
397	collagen type VI alpha 1(COL6A1)	X15880	3	0.02%	2	0.01%
398	KIAA1077	AB029000.1	3	0.02%	2	0.01%
399	SWI/SNF related, matrix associated (SMARCA1)	gi4507066	3	0.02%	2	0.01%
400	ornithine aminotransferase	M29927	3	0.02%	2	0.01%
401	reticulocalbin 2, EF-hand calcium binding domain (RCN2) =X78669 (ORF)	NM_002902.1	3	0.02%	2	0.01%
402	KIAA0143 gene	D63477.1	3	0.02%	2	0.01%
403	myristoylated alanine-rich C-kinase substrate (=D10522 80K-L protein)	M68956	3	0.02%	2	0.01%
404	laminin, alpha 4 (LAMA4)	NM_002290.1	3	0.02%	2	0.01%
405	vascular endothelial growth factor (VEGF)	AF024710.1	3	0.02%	2	0.01%
406	RNA-binding protein regulatory subunit	AF021819	3	0.02%	2	0.01%
407	ATP SYNTHASE A CHAIN (PROTEIN 6)(ORF)	P00846	3	0.02%	2	0.01%
408	S100 calcium-binding protein A13 (S100A13)	NM_005979.1	3	0.02%	2	0.01%
409	glucocorticoid receptor AF-1 specific elongation factor	AF174496.1	3	0.02%	2	0.01%
410	complement factor H (=M17517)	Y00716	2	0.01%	2	0.01%
411	SPARC-like 1 (mast9, hevln) (SPARCL1)	NM_004684.1	2	0.01%	2	0.01%
412	vacuolar sorting protein VPS29/PEP11 (LOC51699)	NM_016226.1	2	0.01%	2	0.01%
413	UDP-glucose dehydrogenase (UGDH)	AF061016	2	0.01%	2	0.01%

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Figure 15 - Relative EST Frequency of Unique Known Genes Common to Fetal and Normal cDNA Libraries - Page 9 of 17

414 SET translocation (myeloid leukemia-associated) (SET) =M93651	NM_003011.1	2	0.01%	2	0.01%
415 HSPC035 protein (LOC51669), NPD003	NM_016127.1	2	0.01%	2	0.01%
416 karyopherin alpha 4 (=importin alpha 3) (KPNA4)	NM_002268.1	2	0.01%	2	0.01%
417 CYTOCHROME C OXIDASE POLYPEPTIDE II	spP00403	2	0.01%	2	0.01%
418 apoptosis related protein APR-1	AF143235.2	2	0.01%	2	0.01%
419: HSPC194	AF151028.1	2	0.01%	2	0.01%
420 KDELF (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor	NM_008854.2	2	0.01%	2	0.01%
421 poly(rC)-binding protein 1 (PCBP1)	NM_008196.1	2	0.01%	2	0.01%
422 immunoglobulin lambda gene	D87003.1	2	0.01%	2	0.01%
423 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8 (19kD, ASH1) (N	NM_005004.1	2	0.01%	2	0.01%
424 cyclophilin-related protein (NKTR) gene (=PAC RPC14-613B23)	AF184110.1	2	0.01%	2	0.01%
425 chaperonin containing T-complex subunit 6 (CCT6) = L27706.1	NM_001762.1	2	0.01%	2	0.01%
426 low density lipoprotein receptor	L00352	2	0.01%	2	0.01%
427 chaperonin containing TCP1 subunit 4 (delta) (CCT4)	NM_008430.1	2	0.01%	2	0.01%
428 translocase of outer mitochondrial membrane 20 (yeast) homolog (KIAA00	NM_014765.1	2	0.01%	2	0.01%
429 serine/threonine kinase KPM	AF207547.1	2	0.01%	2	0.01%
430 alcohol dehydrogenase, class III (ADH5) chi subunit	M30471	2	0.01%	2	0.01%
431 phosphatidic acid phosphatase 2a	AB000888	2	0.01%	2	0.01%
432 KIAA0670 protein/acinusL (no-exact match 42% a.a.)	NP_055792.1	2	0.01%	2	0.01%
433 aspartyl-tRNA synthetase (DARS)	NM_001349.1	2	0.01%	2	0.01%
434 cystatin B	U46692	2	0.01%	2	0.01%
435 cytoplasmic beta-actin	M10277	2	0.01%	2	0.01%
436 YEAH1 (YY1 and E4TF1 associated factor 1)	AB029551.1	2	0.01%	2	0.01%
437 Zn-15 transcription factor (Zfp-15) (=AB011102 Human KIAA0530)	AF017806	2	0.01%	2	0.01%
438 proteasome (prosome, macropain) subunit, beta type, 7 (PSMB7)	NM_002799.1	2	0.01%	2	0.01%
439 gelsolin, plasma (GSN)	X04412	2	0.01%	2	0.01%
440 C9ORF3	AF043897.1	2	0.01%	2	0.01%
441 splicing factor 3b, subunit 2, 145kD (SF3B2)	NM_006842.1	2	0.01%	2	0.01%
442 splicing factor, arginine/serine-rich 4 (SFRS4)	NM_005626.1	2	0.01%	2	0.01%
443 CGI-120 protein (LOC51644)	NM_016057.1	2	0.01%	2	0.01%
444 tumor antigen (L6)	M90657.1	2	0.01%	2	0.01%
445 heat shock factor binding protein 1 (HSBP1)	NM_001537.1	1	0.01%	2	0.01%
446 15 kDa selenoprotein (SEP15)	AF051894	1	0.01%	2	0.01%
447 epidermal growth factor receptor kinase substrate (Eps8)	U12535	1	0.01%	2	0.01%
448 Down syndrome candidate region 1 (DSCR1)	NM_004414.2	1	0.01%	2	0.01%
449 matrilin-2 precursor	U69263	1	0.01%	2	0.01%
450 CYTOCHROME C OXIDASE POLYPEPTIDE I	P00395	1	0.01%	2	0.01%
451 KIAA0663	AB014563	1	0.01%	2	0.01%
452 palmitoyl-protein thioesterase (PPT)	AF022211	1	0.01%	2	0.01%
453 KIAA0102	D14658	1	0.01%	2	0.01%
454 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5 (13kD, B13) (N	NM_005000.1	1	0.01%	2	0.01%
455 GW128	AF107408	1	0.01%	2	0.01%
456 SLC11A3 iron transporter	AF215636.1	1	0.01%	2	0.01%
457 esterase D	AF112219	1	0.01%	2	0.01%
458 DRP-2 dihydropyrimidinase related protein 2	AB020777.1	1	0.01%	2	0.01%
459 KIAA0530	AB011102	1	0.01%	2	0.01%
460 ribosomal protein L33-like protein	AF047440	1	0.01%	2	0.01%
461 synaptophysin-like protein (SYPL)	gi5803184	1	0.01%	2	0.01%
462 conserved gene amplified in osteosarcoma (OS4)	NM_005730.1	1	0.01%	2	0.01%
463 DNA-binding protein A gene	L29073.1	1	0.01%	2	0.01%
464 YME1 (S.cerevisiae)-like 1(YME1L1), = AJ132637.1 ATP-dependent metal	NM_014263.1	1	0.01%	2	0.01%
465 jumping translocation breakpoint (JTB) =AB016488 hJTB (ORF)	NM_006694.1	1	0.01%	2	0.01%

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Figure 14 - Relative EST Frequency of Unique Known Genes Common to Fetal and Normal cDNA Libraries - Page 10 of 17

466	MHC class 1 region	AF055066	1	0.01%	2	0.01%
467	plastin 3 (T isoform) (PLS3)	NM_005032.2	1	0.01%	2	0.01%
468	fibroblast growth factor 2 (basic)(FGF2)	NM_002006.1	1	0.01%	2	0.01%
469	NADH dehydrogenase(ubiquinone) 1, alpha/beta subcomplex, 1 (8kD, SD)	NM_005003.1	1	0.01%	2	0.01%
470	steroid sensitive gene-1 protein (SSG-1)	AF223677.1	1	0.01%	2	0.01%
471	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4	P03905	1	0.01%	2	0.01%
472	PROS-27	X59417	1	0.01%	2	0.01%
473	prolylcarboxypeptidase (angiotensinase C) (PRCP)	NM_005040.1	1	0.01%	2	0.01%
474	GLI-Kruppel family member GLI3 (Greig cephalopolysyndactyly syndrome)	gl4504014	1	0.01%	2	0.01%
475	zinc finger protein 84 (HPF2) (ZNF84)	NM_003428.1	1	0.01%	2	0.01%
476	oxysterol-binding protein	AB017028	1	0.01%	2	0.01%
477	translation initiation factor (=D21853 hypothetical protein (KIAA0111))	X79538	1	0.01%	2	0.01%
478	prostate cancer tumor suppressor (N33)	NM_006785.1	1	0.01%	2	0.01%
479	cytoskeletal tropomyosin TM30(nm)	X04588.1	1	0.01%	2	0.01%
480	capping protein (actin filament) muscle Z-line, alpha 2 (CAPZA2)	NM_006136.1	1	0.01%	2	0.01%
481	chaperonin containing TCP1, subunit 8 (theta) (CCT8)(ORF)	NM_006585.1	1	0.01%	2	0.01%
482	Integrin, alpha E (antigen CD103, human mucosal lymphocyte antigen 1; a	NM_002208.3	1	0.01%	2	0.01%
483	chondrosarcoma-associated protein 2 (CSA2)	AF182645.1	1	0.01%	2	0.01%
484	housekeeping (Q1Z 7F5) gene	M81806.1	1	0.01%	2	0.01%
485	KIAA0871	AB014571.1	1	0.01%	2	0.01%
486	KIAA1376 protein	AB037797.1	1	0.01%	2	0.01%
487	serine palmitoyl transferase	AF111168.2	1	0.01%	2	0.01%
488	NADH-ubiquinone oxidoreductase B17	AF067167.1	1	0.01%	2	0.01%
489	basic transcription factor 3 (RefSeq aa 4e-39)	NP_001198.1	1	0.01%	2	0.01%
490	CGI-74 protein	AF151832.1	1	0.01%	2	0.01%
491	coxsackievirus and adenovirus receptor (CXADR)	AF200465.1	1	0.01%	2	0.01%
492	insulin receptor	L07782	1	0.01%	2	0.01%
493	leptin receptor (ORF)	U66496	1	0.01%	2	0.01%
494	protein-kinase, interferon-inducible double stranded RNA dependent inhibit	NP_006251.1	1	0.01%	2	0.01%
495	high-glucose-regulated protein 8 (HGRG8)	AF192988.1	1	0.01%	2	0.01%
496	prefoldin 1 (PFDN1)	NM_002622.1	1	0.01%	2	0.01%
497	KIAA0993	AB023210.1	1	0.01%	2	0.01%
498	Nijmegen breakage syndrome 1 (nibrin) (NBS1)	NM_002485.2	1	0.01%	2	0.01%
499	topoisomerase IIb mRNA,(= TOP2 mRNA for DNA topoisomerase II)	U54831.1	1	0.01%	2	0.01%
500	CUG triplet repeat RNA-binding protein 2 (CUGBP2), (=apoptosis-related F	NM_006561.1	1	0.01%	2	0.01%
501	galactosidase, alpha (GLA)	NM_000169.1	1	0.01%	2	0.01%
502	methionine adenosyltransferase alpha subunit	L43509	1	0.01%	2	0.01%
503	cysteine protease	D55696.1	1	0.01%	2	0.01%
504	six transmembrane epithelial antigen of prostate (STEAP1)	AF186249.1	1	0.01%	2	0.01%
505	GTT1	AF270647	1	0.01%	2	0.01%
506	HSPC033 protein (HSPC033)	NM_014041.1	1	0.01%	2	0.01%
507	retinal pigment epithelium	L07393.1	1	0.01%	2	0.01%
508	pyrroline-5-carboxylate reductase 1 (PYCR1)	NM_006907.1	1	0.01%	2	0.01%
509	S-adenosylmethionine decarboxylase 1 (AMD1)	NM_001634.3	1	0.01%	2	0.01%
510	sorting nexin 1 (SNX1)	NM_003099.1	1	0.01%	2	0.01%
511	TRAM-like protein (KIAA0057), mRNA	NM_012288.1	1	0.01%	2	0.01%
512	bromodomain-containing 2 (BRD2)= KIAA9001	NM_005104.1	1	0.01%	2	0.01%
513	laminin, beta 2 (laminin S)(LAMB2) mRNA	NM_002292.1	1	0.01%	2	0.01%
514	glutamate dehydrogenase 1 (GLUD1)	NM_005271.1	1	0.01%	2	0.01%
515	leptin receptor gene-related protein (HSOBRGRP)	NM_017526.1	1	0.01%	2	0.01%
516	Ser/Arg-related nuclear matrix protein (plenty of prolines 101-like) (SRM16	NM_005839.1	1	0.01%	2	0.01%
517	serum-inducible kinase (SNK)	AF223574.1	1	0.01%	2	0.01%

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Figure 15 - Relative EST Frequency of Unique Known Genes Common to Fetal and Normal cDNA Libraries - Page 11 of 17

518	quiescin Q6 (QSCN6)(= bone-derived growth factor (BPGF-1))	NM_002828.1	1	0.01%	2	0.01%
519	brain-specific STE20-like protein kinase 3 (STK3)	AF083420.1	1	0.01%	2	0.01%
520	Sec31 protein	AF139184.1	1	0.01%	2	0.01%
521	high-mobility group (nonhistone chromosomal) protein 14 (HMG14)	NM_004965.1	1	0.01%	2	0.01%
522	ribosomal protein, large, P1 (RPLP1)	NM_001003.1	40	0.30%	1	0.01%
523	ribosomal protein S28, yeast homologue	D14530	38	0.28%	1	0.01%
524	ribosomal protein S18	X69150.1	33	0.25%	1	0.01%
525	ribosomal protein L18 (RPL18)	NM_000979.1	28	0.21%	1	0.01%
526	ribosomal protein L18a	L05093.1	27	0.20%	1	0.01%
527	H19 (=PRO2605)	M32053	25	0.19%	1	0.01%
528	RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN)	spP15880	24	0.18%	1	0.01%
529	ribosomal protein S10	NM_001014.1	22	0.16%	1	0.01%
530	ribosomal protein L29 (RPL29)	NM_000992.1	21	0.16%	1	0.01%
531	elongation factor 2	X51486	16	0.12%	1	0.01%
532	aggrecan (chondroitin sulfate proteoglycan 1, large aggregating proteoglycan)	U13613	14	0.10%	1	0.01%
533	dolichyl-phosphate beta-glucosyltransferase (ALG5)	AF102850.1	13	0.10%	1	0.01%
534	calcydin (=M14300 growth factor-inducible 2A9 gene; U04815 protein kinase)	J02763	10	0.07%	1	0.01%
535	mesoderm specific transcript (mouse) homolog (MEST)	NM_002402.1	10	0.07%	1	0.01%
536	androgen receptor associated protein 24 (ARA24) (=AF054183 GTP binding protein)	AF052578	8	0.06%	1	0.01%
537	transmembrane protein (p63)	X69910	8	0.06%	1	0.01%
538	ATP synthase, H transporting, mitochondrial F1F0, subunit g (ATP5JG)	NM_008476.1	7	0.05%	1	0.01%
539	ADP-ribosylation factor 1	M84326.1	7	0.05%	1	0.01%
540	melanoma-associated antigen MG50	AF200348.1	7	0.05%	1	0.01%
541	phosphoglycerate mutase (PGAM-B)	J04173	6	0.04%	1	0.01%
542	transcription factor BTF 3	X74070	6	0.04%	1	0.01%
543	DEK oncogene (DNA binding) (DEK)	gi4503248	5	0.04%	1	0.01%
544	titin (TTN) gene	CAA49245.1	5	0.04%	1	0.01%
545	ISLR (immunoglobulin superfamily containing leucine-rich repeat) gene,	AB024537	5	0.04%	1	0.01%
546	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV)	NM_001897.1	5	0.04%	1	0.01%
547	shox gene	U82668	5	0.04%	1	0.01%
548	high mobility group-1 protein (HMG-1)	X12597	4	0.03%	1	0.01%
549	collagen type V alpha 2 (COL5A2)	M11718	4	0.03%	1	0.01%
550	cyclin	M74091	4	0.03%	1	0.01%
551	sphingolipid activator protein 1	J03015	4	0.03%	1	0.01%
552	non-metastatic cells 2, protein (NM23B) expressed in (NME2)	NM_002512.1	4	0.03%	1	0.01%
553	filamin (FLNB)	AF191633.1	4	0.03%	1	0.01%
554	H3 histone, family 3B (H3.3B) (H3F3B)	NM_005324.1	4	0.03%	1	0.01%
555	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (PF2K) (=AB00790)	AF041832	4	0.03%	1	0.01%
556	ornithine decarboxylase antizyme	D87914	4	0.03%	1	0.01%
557	myeloid leukemia factor 2 (MLF2)	NM_005439.1	4	0.03%	1	0.01%
558	PRO2605	AF116709.1	4	0.03%	1	0.01%
559	Cu/Zn superoxide dismutase (SOD)	X02317	3	0.02%	1	0.01%
560	YAP65	X80507.1	3	0.02%	1	0.01%
561	prolyl 4-hydroxylase gene	U14608.1	3	0.02%	1	0.01%
562	protein phosphatase 2A catalytic subunit-beta	M60484	3	0.02%	1	0.01%
563	ubiquitin gene	U49869	3	0.02%	1	0.01%
564	Arp2/3 protein complex subunit p16 (ARC16) =AF008088 (ORF)	NM_005717.1	3	0.02%	1	0.01%
565	eukaryotic translation initiation factor 3, subunit 3 (gamma, 40kD)	gi4503514	3	0.02%	1	0.01%
566	zinc finger protein SLUG (SLUG) gene	AF084243.1	3	0.02%	1	0.01%
567	KIAA0038 gene	D26088.1	3	0.02%	1	0.01%
568	U50HG genes for U50' snoRNA and U50 snoRNA, complete sequence	AB017710	3	0.02%	1	0.01%
569	RAD21 (S. pombe) homolog (RAD21) (=X98294)	gi5453993	3	0.02%	1	0.01%

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Figure 14 - Relative EST Frequency of Unique Known Genes Common to Fetal and Normal cDNA Libraries - Page 12 of 17

570	transformer-2 alpha (htra-2 alpha)	U53209.1	3	0.02%	1	0.01%
571	karyopherin (importin) beta 1 (KPNB1) (=L38951 importin beta subunit)	gi4504904	3	0.02%	1	0.01%
572	endothelial differentiation-related factor 1 (EDF1)	NM_003792.1	3	0.02%	1	0.01%
573	G8 protein (G8)	NM_016947.1	3	0.02%	1	0.01%
574	KIAA0107	D14863	3	0.02%	1	0.01%
575	KIAA0325 gene	AB002323.1	3	0.02%	1	0.01%
576	xeroderma pigmentosum group E UV-damaged DNA binding factor = NM_032986.1	U32986.1	3	0.02%	1	0.01%
577	replication factor C (activator 1) 1 (145kD) (RFC1) mRNA	NM_002913.1	3	0.02%	1	0.01%
578	hexokinase 1 (HK1) (=AF016365;X68957)	M75126	3	0.02%	1	0.01%
579	DNA-dependent protein kinase catalytic subunit (DNA-PKcs)	U47077.3	3	0.02%	1	0.01%
580	nucleosome assembly protein 1-like 1 (NAP1L1)	XM_047969.1	3	0.02%	1	0.01%
581	MHC class I (HLA-A)	U59701	3	0.02%	1	0.01%
582	signal sequence receptor, beta (translocon-associated protein beta) (SSR2.X74104)	U59701	3	0.02%	1	0.01%
583	KIAA0251	D87438	3	0.02%	1	0.01%
584	eIF4E-like cap-binding protein (4EHP) (=translation initiation factor 4e)	NM_004846.1	3	0.02%	1	0.01%
585	RNA binding motif protein 5 (RBM5)	AF091263.1	3	0.02%	1	0.01%
586	isolate Liv chaperone protein HSP90 beta (HSP90BETA)	AF275719.1	3	0.02%	1	0.01%
587	echinoderm microtubule-associated protein homolog HuEMAP	U97018	3	0.02%	1	0.01%
588	endozepine (putative ligand of benzodiazepine receptor)	M15887.1	2	0.01%	1	0.01%
589	RAN, member RAS oncogene family (RAN), mRNA /cds=(114,764) /gb=NM_10842	U97018	2	0.01%	1	0.01%
590	actin-related protein Arp3 (ARP3)(actin-related protein 3 yeast)homolog(AcAF006083.1)	AF006083.1	2	0.01%	1	0.01%
591	biglycan BGN	U11686.1	2	0.01%	1	0.01%
592	Eukaryotic translation initiation factor 2, subunit 2 (beta, 38kD)(EIF2S2)	NM_003908.1	2	0.01%	1	0.01%
593	CGI-149 protein	AF151907.1	2	0.01%	1	0.01%
594	basic transCRiption factor 2 p44 (btf2p44) gene, partial cds, neuronal apop	U80017.1	2	0.01%	1	0.01%
595	CD35 antigen	L06850.1	2	0.01%	1	0.01%
596	KIAA0436	AB007896	2	0.01%	1	0.01%
597	growth arrest specific transCRipt 5 gene	AF141346.1	2	0.01%	1	0.01%
598	ARP2/3 protein complex subunit 34 (ARC34)	NM_005731.1	2	0.01%	1	0.01%
599	high mobility group 2 protein (HMG-2)	M83665	2	0.01%	1	0.01%
600	pyruvate dehydrogenase (lipoamide) alpha 1 (PDHA1)	NM_000284.1	2	0.01%	1	0.01%
601	sarcoglycan, beta (43kD dystrophin-associated glycoprotein) (SGCB)	NM_000232.1	2	0.01%	1	0.01%
602	tubulin-specific chaperone a (TBCA) (=AF038952 cofactor A protein)	gi4759211	2	0.01%	1	0.01%
603	KIAA0810	AB018353.1	2	0.01%	1	0.01%
604	fatty acid binding protein 5 (psoriasis-associated) (FABP5)	NM_001444.1	2	0.01%	1	0.01%
605	ubiquinol-cytochrome c reductase core protein II (UQCRC2)(ORF) = J0497	NM_003366.1	2	0.01%	1	0.01%
606	phosphoglycerate mutase 1 (brain) (PGAM1), mRNA /cds=(31,795) /gb=NM_181013	U80017.1	2	0.01%	1	0.01%
607	enhancer of polycomb (Epc1)	AF079765	2	0.01%	1	0.01%
608	KIAA0138	D50926.1	2	0.01%	1	0.01%
609	ubiquinol-cytochrome c reductase (6.4kD) subunit (UQCR)	NM_008830.1	2	0.01%	1	0.01%
610	proteasome-associated pad1 homologue (POH1) 26S	U86782	2	0.01%	1	0.01%
611	cathepsin F (CATSF)	AF071749	2	0.01%	1	0.01%
612	membrane component, chromosome 11, surface marker 1 (M11S1) = Z480	NM_005898.1	2	0.01%	1	0.01%
613	signal transducer and activator of transcription 1, 91kD (STAT1)(=transcrip	NM_007315.1	2	0.01%	1	0.01%
614	cyclin D2(=KIAA0002 gene)	NM_001759.1	2	0.01%	1	0.01%
615	deoxyuridine triphosphatase(DUT) mRNA, complete cds	U62891.1	2	0.01%	1	0.01%
616	cysteinyl-tRNA synthetase	L06845.1	2	0.01%	1	0.01%
617	smooth muscle myosin alkali light chain	U02629.1	2	0.01%	1	0.01%
618	DiGeorge syndrome critical region gene 6 (DGCR6)	NM_005875.1	2	0.01%	1	0.01%
619	cold inducible RNA-binding protein (CIRBP)	NM_001280.1	2	0.01%	1	0.01%
620	HSPC037 protein (LOC51659)	NM_016095.1	2	0.01%	1	0.01%
621	nuclear distribution gene C (Anidulans) homolog (NUDC)	NM_006600.1	2	0.01%	1	0.01%

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Figure 18 - Relative EST Frequency of Unique Known Genes Common to Fetal and Normal cDNA Libraries - Page 13 of 17

622	thiosulfate sulfurtransferase (rhodanese) (TST)	X59434	2	0.01%	1	0.01%
623	TL27 (from PC3 cell line)	X75684	2	0.01%	1	0.01%
624	WW domain binding protein-1 (ORF)	U79457.17	2	0.01%	1	0.01%
625	acyl-Coenzyme A dehydrogenase, very long chain (ACADVL), nuclear gene	NM_000018.1	2	0.01%	1	0.01%
626	transducin (beta) like 2 (TBL2)	NM_012453.1	2	0.01%	1	0.01%
627	small nuclear ribonucleoprotein polypeptide F (SNRPF)	NM_003095.1	2	0.01%	1	0.01%
628	coatamer protein complex, subunit alpha (COPA), mRNA	NM_004371.2	2	0.01%	1	0.01%
629	sorcin (SRI)	L12387.1	2	0.01%	1	0.01%
630	capping protein (actin filament), gelsolin-like (CAPG)	M94345	2	0.01%	1	0.01%
631	inositol 1,4,5-triphosphate receptor, type 3 (ITPR3)	U01062	2	0.01%	1	0.01%
632	interleukin 11 receptor, alpha (IL11RA)	NM_004512.1	2	0.01%	1	0.01%
633	EGR1 gene for early growth response protein 1 (=zinc finger protein)(= trans	AJ243425.1	2	0.01%	1	0.01%
634	coatamer protein (COPA)	U24105	2	0.01%	1	0.01%
635	mimiccan (OGN) (OIF)	AF202167.1	1	0.01%	1	0.01%
636	MAFB/Kreisler basic region/leucine zipper transcription factor (MAFB)	AF134157.1	1	0.01%	1	0.01%
637	Ku autoimmune antigen gene	J04877.1	1	0.01%	1	0.01%
638	myosin light chain 3 non-muscle (MLC3nm)	M31212	1	0.01%	1	0.01%
639	ARP2/3 protein complex subunit p21 (ARC21=AF006086 (ORF)	NM_005719.1	1	0.01%	1	0.01%
640	NS1-binding protein (NS1-BP) (=AB020657 KIAA0850)	AJ012449	1	0.01%	1	0.01%
641	inositol polyphosphate 1-phosphatase gene (INPP1) (low match)	AF141324.1	1	0.01%	1	0.01%
642	uridine diphosphoglucose pyrophosphorylase	U27460	1	0.01%	1	0.01%
643	UDP-glucose pyrophosphorylase 2 (ORF)	NM_006759.1	1	0.01%	1	0.01%
644	KIAA0332	AB002330	1	0.01%	1	0.01%
645	ras-related GTP-binding protein	AF106681.1	1	0.01%	1	0.01%
646	non-histone chromosomal protein (HMG-1)	L08048.1	1	0.01%	1	0.01%
647	lysosomal-associated membrane glycoprotein-1 (LAMP1) (=J04182)	L08582	1	0.01%	1	0.01%
648	oomichon protein	AF070654.1	1	0.01%	1	0.01%
649	KIAA0766	AB018309.1	1	0.01%	1	0.01%
650	Id-2H	D13891	1	0.01%	1	0.01%
651	transcription factor (CBFB)	L20298	1	0.01%	1	0.01%
652	KIAA1025	AB028948.1	1	0.01%	1	0.01%
653	LGMD2B	AJ007973	1	0.01%	1	0.01%
654	KIAA0103	D14659	1	0.01%	1	0.01%
655	basic helix-loop-helix domain containing, class B, 2 (BHLHB2), mRNA /cds	Hs.171825	1	0.01%	1	0.01%
656	eukaryotic translation initiation factor 3, subunit 10 (theta, 150/170kD)	gi4503508	1	0.01%	1	0.01%
657	protein kinase C inhibitor-1	U27143	1	0.01%	1	0.01%
658	heterogeneous nuclear ribonucleoprotein R (ORF)	AF000364	1	0.01%	1	0.01%
659	growth arrest and DNA-damage-inducible, alpha (GADD45A)	NM_001924.1	1	0.01%	1	0.01%
660	KIAA0077 gene	D38521.1	1	0.01%	1	0.01%
661	CYTOCHROME C OXIDASE POLYPEPTIDE III	P00414	1	0.01%	1	0.01%
662	farnesyl-protein transferase alpha-subunit	L00634	1	0.01%	1	0.01%
663	Polyadenylate binding protein	U75688.1	1	0.01%	1	0.01%
664	Splicing factor proline/glutamine rich (polypyrimidine tract-binding protein-a	NM_005066.1	1	0.01%	1	0.01%
665	myosin class I, myh-1c	AJ001382	1	0.01%	1	0.01%
666	activin A receptor, type I (ACVR1) =Z22534 ALK-2	NM_001105.1	1	0.01%	1	0.01%
667	KIAA1058 protein	AB028981.1	1	0.01%	1	0.01%
668	tetraspan TM4SF(TSPAN-6)	AF053453	1	0.01%	1	0.01%
669	Rosenthal fiber protein (alpha-B-Crystallin)	M24908	1	0.01%	1	0.01%
670	ring finger protein 4 (RNF4)	gi4508560	1	0.01%	1	0.01%
671	nuclear factor (erythroid-derived 2)-like 2 (NFE2L2) (=S74017 Nr2=NF-E2	gi5453775	1	0.01%	1	0.01%
672	myosin-binding protein C, cardiac (MYBPC3)	NM_000256.1	1	0.01%	1	0.01%
673	IQ motif containing GTPase activating protein 1 (IQGAP1)	NM_003870.1	1	0.01%	1	0.01%

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Figure 14 - Relative EST Frequency of Unique Known Genes Common to Fetal and Normal cDNA Libraries - Page 14 of 17

674	ATP synthase, H ⁺ transporting, mitochondrial F0 complex, subunit f, isoform	NM_004889.1	1	0.01%	1	0.01%
675	cytochrome c oxidase subunit Vb (coxVb)	M19981	1	0.01%	1	0.01%
676	hect domain and RLD 2(HERC2) (=KIAA0393)	NM_004667.2	1	0.01%	1	0.01%
677	integrin cytoplasmic domain associated protein (Icap-1a)	AF012023	1	0.01%	1	0.01%
678	KIAA0235	D87078	1	0.01%	1	0.01%
679	KIAA0252	D87440	1	0.01%	1	0.01%
680	KIAA0693	AB014593	1	0.01%	1	0.01%
681	nickel-specific induction protein (Cap43)	AF004162.1	1	0.01%	1	0.01%
682	PRO1608	AF119850.1	1	0.01%	1	0.01%
683	phosphoribosyl pyrophosphate synthetase subunit I	D00860.1	1	0.01%	1	0.01%
684	phospholipid sCRamblase 1 PLSCR1	AF098642	1	0.01%	1	0.01%
685	cytochrome oxidase subunit I (COI) and subunit II (COII) pseudogenes	AF035429.1	1	0.01%	1	0.01%
686	wbsCR1 (WBSCR1)	AF045555.1	1	0.01%	1	0.01%
687	proteasome (prosome, macropain) subunit, alpha type, 3 (PSMA3)	NM_002786.1	1	0.01%	1	0.01%
688	CLP (CLPP)	LS4057.1	1	0.01%	1	0.01%
689	platelet-activating factor acetylhydrolase, isoform 1b, alpha subunit (PAFAH)	4557740	1	0.01%	1	0.01%
690	P311 protein (P311), mRNA /cds=(202,408) /gb=Nm_004772 /gi=4758865	Hs.142827	1	0.01%	1	0.01%
691	small EDRK-rich factor 1, long isoform (SERF1) (=btf2p44)	AF073519.1	1	0.01%	1	0.01%
692	KIAA0592 (ORF)	AB011184	1	0.01%	1	0.01%
693	lysophospholipase (LPL1)	AF081281	1	0.01%	1	0.01%
694	KARP-1-binding protein 3 (=KIAA0470)	AB022659.1	1	0.01%	1	0.01%
695	inducible 6-phosphofructo-2-kinase/fructose 2,6-bisphosphatase (IPFK-2)	AF056320	1	0.01%	1	0.01%
696	reticulocalbin 1, EF-hand calcium binding domain (RCN1)	NM_002901.1	1	0.01%	1	0.01%
697	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5 (16kD, SGD1)	NM_002492.1	1	0.01%	1	0.01%
698	major histocompatibility complex, class II, DR beta 1 (HLA-DRB1)	NM_002124.1	1	0.01%	1	0.01%
699	nerve growth factor (HBNF-1)(= OSF-1)(= pleiotropin)	M57399.1	1	0.01%	1	0.01%
700	ras-related C3 botulinum toxin substrate (rac)	M29870	1	0.01%	1	0.01%
701	HSPC328	AF161446.1	1	0.01%	1	0.01%
702	Glutathione transferase omega (GSTO1)	AF212303.1	1	0.01%	1	0.01%
703	NRAS-related gene (D1S155E) (=DKFZp586J0620)	NM_007158.1	1	0.01%	1	0.01%
704	RAB13, member RAS oncogene family (RAB13) mRNA	NM_002870.1	1	0.01%	1	0.01%
705	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1 (6kD, KFY1)	NM_002494.1	1	0.01%	1	0.01%
706	NADH dehydrogenase (ubiquinone) Fe-S protein 6 (13kD) (NADH-coenzyme	NM_004553.1	1	0.01%	1	0.01%
707	Na,K-ATPase beta subunit (ATP1B)	M25160	1	0.01%	1	0.01%
708	retinoblastoma-binding protein 7 (RBBP7)	NM_002893.1	1	0.01%	1	0.01%
709	zinc finger protein 133 (clone pHZ-13) (ZNF133)	NM_003434.1	1	0.01%	1	0.01%
710	retinoic acid suppression protein A (RSG-A)	AF038964.1	1	0.01%	1	0.01%
711	latent transforming growth factor beta binding protein 2 (LTBP2)	NM_000428.1	1	0.01%	1	0.01%
712	fer-1 (C. elegans)-like 3 (FER1L3) (=AF182317 myoferlin (MYOF))	NM_013451.1	1	0.01%	1	0.01%
713	telomeric repeat binding factor (TRF1)	U40705.1	1	0.01%	1	0.01%
714	prefoldin 2 (PFDN2)	NM_012394.1	1	0.01%	1	0.01%
715	ELK1 (ELK1)	AF080818	1	0.01%	1	0.01%
716	HSPC162 protein (HSPC162)	NM_014183.1	1	0.01%	1	0.01%
717	HSPC218	AF151052.1	1	0.01%	1	0.01%
718	HSPC337	AF161455.1	1	0.01%	1	0.01%
719	iduronate sulphate sulphatase (IDS) gene	L35485.1	1	0.01%	1	0.01%
720	KIAA0081	D42039	1	0.01%	1	0.01%
721	KIAA0099 protein, partial cds	D43951.1	1	0.01%	1	0.01%
722	KIAA0152 (cytotoxic T-cell membrane glycoprotein Ly-3 isolog)	NM_014730.1	1	0.01%	1	0.01%
723	KIAA0188	D80010	1	0.01%	1	0.01%
724	KIAA0419 gene product (KIAA0419)	NM_014711.1	1	0.01%	1	0.01%
725	KIAA0458	AB007927.1	1	0.01%	1	0.01%

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Figure 18 - Relative EST Frequency of Unlque Known Genes Common to Fetal and Normal cDNA Libraries - Page 15 of 17

726	KIAA0484	AB007953.1	1	0.01%	1	0.01%
727	KIAA0698 protein	AB014598	1	0.01%	1	0.01%
728	KIAA0851 gene	AJ297357.1	1	0.01%	1	0.01%
729	KIAA1182	AB032988.1	1	0.01%	1	0.01%
730	channel-like integral membrane protein (AQP-1)	U41518.1	1	0.01%	1	0.01%
731	cltrln (SLC25A13)	AF118838.1	1	0.01%	1	0.01%
732	L3 pigment (L3)	AF189062.3	1	0.01%	1	0.01%
733	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1 (UQCR)	5174742	1	0.01%	1	0.01%
734	matrix metalloprotease(ADAMTS1) mRNA, complete cds	AF207664.1	1	0.01%	1	0.01%
735	myocyte-specific enhancer factor 2A (MEF2A)	U49020	1	0.01%	1	0.01%
736	retinoblastoma-binding protein 4 (RBBP4) =X74262 RbAp48	NM_005610.1	1	0.01%	1	0.01%
737	T-box transCRiption factor (Tbx15)	AF041822	1	0.01%	1	0.01%
738	Y-linked zinc finger protein (ZFY) gene (=DKFZp434F2311)	AF114156.1	1	0.01%	1	0.01%
739	polyadenylate binding protein(TIA-1)	M77142	1	0.01%	1	0.01%
740	tetraspanin TM4-A	AF133423.1	1	0.01%	1	0.01%
741	calponin 3, acidic (CNN3)	NM_001839.1	1	0.01%	1	0.01%
742	nonmuscle myosin heavy chain (NMHC)	M31013	1	0.01%	1	0.01%
743	glucocorticoid receptor (GRL) gene	U80947.1	1	0.01%	1	0.01%
744	CDC-like kinase (CLK)	NM_004071.1	1	0.01%	1	0.01%
745	tyrosylprotein sulfotransferase-1(TPST1)	AF038009	1	0.01%	1	0.01%
746	GTPase-activating protein ras p21 (RASA)	M23379	1	0.01%	1	0.01%
747	CC chemokine gene cluster	AF088219.1	1	0.01%	1	0.01%
748	ARP2 (actin-related protein 2, yeast) homolog (ACTR2)	NM_005722.1	1	0.01%	1	0.01%
749	cdk inhibitor p21 binding protein (TOK-1),(ORF)= AB040450.1	NM_016567.1	1	0.01%	1	0.01%
750	KIAA0160	D63881	1	0.01%	1	0.01%
751	PRO0989	AF116614	1	0.01%	1	0.01%
752	transposon-like element	M23161	1	0.01%	1	0.01%
753	WSB1 isoform 2 (WSB1)	AF240696.1	1	0.01%	1	0.01%
754	UDP-N-acetyl-alpha-D-galactosamine:polypeptide	NM_004481.1	1	0.01%	1	0.01%
755	Rab5 GDP/GTP exchange factor homologue (RABEX5)	NM_014504.1	1	0.01%	1	0.01%
756	eukaryotic translation Initiation factor 3, subunit 7 (zeta, 66/67kD)	NM_003753.1	1	0.01%	1	0.01%
757	Id3 gene for HLH type transcription factor	X73428.1	1	0.01%	1	0.01%
758	nuclear autoantigenic sperm protein (histone-binding) (NASP)	NM_002482.1	1	0.01%	1	0.01%
759	APEX nuclease (multifunctional DNA repair enzyme) (RefSeq aa 4e-74)	NP_001632.1	1	0.01%	1	0.01%
760	phosphoribosyl pyrophosphate synthetase-associated protein 1 (PRPSAP1)	NM_002766.1	1	0.01%	1	0.01%
761	low density lipoprotein-related protein 1 (alpha-2-macroglobulin receptor) (L1)	NM_002332.1	1	0.01%	1	0.01%
762	poly(A)-binding protein, nuclear 1 (PABPN1)	gi4758875	1	0.01%	1	0.01%
763	microfibrillar-associated protein 1 (MFAP1)	NM_005926.1	1	0.01%	1	0.01%
764	lamin B receptor (LBR)	NM_002296.1	1	0.01%	1	0.01%
765	guanine nucleotide binding protein 10 (GNG10)	NM_004125.1	1	0.01%	1	0.01%
766	histone H2A.F/Z variant (H2AV)	AF081192	1	0.01%	1	0.01%
767	adipose differentiation-related protein (ADFP)	XM_048266.2	1	0.01%	1	0.01%
768	GL004 protein (RefSeq aa 2e-34)	NP_064579.1	1	0.01%	1	0.01%
769	HDCMC29P	AF088295.1	1	0.01%	1	0.01%
770	HSPC229	AF151063.1	1	0.01%	1	0.01%
771	KIAA0117	D38491	1	0.01%	1	0.01%
772	KIAA0324	AB002322.2	1	0.01%	1	0.01%
773	KIAA0447	AB007916	1	0.01%	1	0.01%
774	KIAA0470	AB007939	1	0.01%	1	0.01%
775	KIAA0488	AB007957.1	1	0.01%	1	0.01%
776	KIAA0770	AB018313.1	1	0.01%	1	0.01%
777	KIAA0772 gene	NM_014835.1	1	0.01%	1	0.01%

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Figure 15 - Relative EST Frequency of Unique Known Genes Common to Fetal and Normal cDNA Libraries - Page 16 of 17

778	KIAA1190	AB033016.1	1	0.01%	1	0.01%
779	KIAA1404	AB037825.1	1	0.01%	1	0.01%
780	KIAA1507(=FLJ20654)	AB040940.1	1	0.01%	1	0.01%
781	MCT-1 protein (MCT-1)	NM_014060.1	1	0.01%	1	0.01%
782	microspherule protein 1 (MCRS1)	NM_006337.1	1	0.01%	1	0.01%
783	neuroblastoma-amplified protein	AF056195	1	0.01%	1	0.01%
784	NICE-5 protein =AF118721) PRO3094	AJ243666	1	0.01%	1	0.01%
785	non-oncogenic Rho GTPase-specific GTP exchange factor (proto-LBC)	AF127481.1	1	0.01%	1	0.01%
786	PTPRF interacting protein, binding protein 1 (liprin beta 1) (RefSeq aa 29-34)	NP_003613.1	1	0.01%	1	0.01%
787	testis specific protein	AF146738.1	1	0.01%	1	0.01%
788	WRN (WRN)	AF181897.1	1	0.01%	1	0.01%
789	sodium calcium exchanger 1 (NCX1)	U83657	1	0.01%	1	0.01%
790	paraoxonase 2 (PON2)	NM_000305.1	1	0.01%	1	0.01%
791	TPH1 gene for triosephosphate isomerase	X69723.1	1	0.01%	1	0.01%
792	adenylosuccinate lyase(ADSL)	NM_000026.1	1	0.01%	1	0.01%
793	purine nucleoside phosphorylase	X00737	1	0.01%	1	0.01%
794	enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase alpha-subunit of	D16480	1	0.01%	1	0.01%
795	dolichyl-phosphate mannosyltransferase polypeptide 1, catalytic subunit (D)	NM_003859.1	1	0.01%	1	0.01%
796	leucine zipper, down-regulated in cancer 1 (LDOC1)	NM_012317.1	1	0.01%	1	0.01%
797	ORNITHINE DECARBOXYLASE (ODC)	spP00860	1	0.01%	1	0.01%
798	alpha-1-antitrypsin	K01396.1	1	0.01%	1	0.01%
799	F-box protein 7 (FBX7)	NM_012179.1	1	0.01%	1	0.01%
800	peroxisomal biogenesis factor 12 (PEX12)	NM_000286.1	1	0.01%	1	0.01%
801	bihoraxoid-like protein (BLP)(= HSPC162 protein (HSPC162))	AF165516.1	1	0.01%	1	0.01%
802	glioma-amplified sequence-41 (GAS41)	NM_006530.1	1	0.01%	1	0.01%
803	B cell RAG associated protein (BRAG) (=AB011170 hypothetical protein (K))	AF026477	1	0.01%	1	0.01%
804	jun D proto-oncogene (JUND)	NM_005354.1	1	0.01%	1	0.01%
805	mel transforming oncogene (derived from cell line NK14)- RAB8 homolog (NM_005370.2)	1	0.01%	1	0.01%	
806	nuclear factor of activated T-cells, cytoplasmic 4 (NFATC4) mRNA	NM_004554.1	1	0.01%	1	0.01%
807	transCRiption factor ETR101	M62831	1	0.01%	1	0.01%
808	M5-14 protein (LOC51300)	NM_016589.1	1	0.01%	1	0.01%
809	splicing factor arginine/serine-rich 7 (SFRS7) gene	L41887.1	1	0.01%	1	0.01%
810	splicing factor similar to dnaJ (SPF31)	NM_014280.1	1	0.01%	1	0.01%
811	splicing factor SRp30c gene	U87279.1	1	0.01%	1	0.01%
812	U5 snRNP-associated 102 kDa protein	AF221842.1	1	0.01%	1	0.01%
813	RNA polymerase I 40kD subunit	AF047441	1	0.01%	1	0.01%
814	EBNA-2 co-activator (100kD) (p100)	NM_014390.1	1	0.01%	1	0.01%
815	brain and reproductive organ-expressed (TNFRSF1A modulator) (BRE)	NM_004899.1	1	0.01%	1	0.01%
816	ALEX3 protein (ALEX3)	NM_016607.1	1	0.01%	1	0.01%
817	beta-subunit signal transducing proteins GS/GI (clone 24596)	AF070697	1	0.01%	1	0.01%
818	carbonyl reductase 1 (CBR1)	NM_001757.1	1	0.01%	1	0.01%
819	thioredoxin-like, 32kD (TXNL)	NM_004786.1	1	0.01%	1	0.01%
820	clathrin heavy chain (=D21260 human hypothetical protein (KIAA0034))	J03583	1	0.01%	1	0.01%
821	sodium-dependent multivitamin transporter (SMVT) gene, partial cds	AF116241.1	1	0.01%	1	0.01%
822	synaptic glycoprotein SC2 spliced variant	AF038958	1	0.01%	1	0.01%
823	microtubule-associated protein 1a (MAP1A)	U38292.1	1	0.01%	1	0.01%
824	platelet-derived growth factor A chain (PDGFA) (=X06374)	M83575	1	0.01%	1	0.01%
825	v-jun avian sarcoma virus 17 oncogene homolog (JUN), (=c-jun proto onco	NM_002228.2	1	0.01%	1	0.01%
826	Rab9 effector p40	Z97074	1	0.01%	1	0.01%
827	Rho guanine nucleotide-exchange factor, splice variant NET1A	AJ010045.1	1	0.01%	1	0.01%
828	p8 protein (candidate of metastasis 1) (P8)	NM_012385.1	1	0.01%	1	0.01%
829	uncharacterized bone marrow protein BM042 (BM042) (=DKFZp761A1124)	NM_018458.1	1	0.01%	1	0.01%

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Figure 15 Relative EST Frequency of Unique Known Genes Common to Fetal and Normal cDNA Libraries - Page 17 of 17

830	cullin 5 (CUL5)	NM_003478.1	1	0.01%	1	0.01%
831	ADP-ribosylation factor 6 (ARF6)	NM_001663.2	1	0.01%	1	0.01%
832	chloride channel nucleotide-sensitive, 1A (CLNS1A)	NM_001283.1	1	0.01%	1	0.01%
833	JTV-1 (JTV-1)	U24169	1	0.01%	1	0.01%
834	membrane protein-like protein	U21556	1	0.01%	1	0.01%
835	integrin alpha-11 subunit precursor (ITGA11)	AF109681.1	1	0.01%	1	0.01%
836	TRAF and TNF receptor associated protein (trap gene)	AJ269473.1	1	0.01%	1	0.01%
837	chromodomain helicase DNA binding protein 4 (CHD4)	NM_001273.1	1	0.01%	1	0.01%
838	Gu protein = PC6010 RNA helicase Gu	U41387.1	1	0.01%	1	0.01%
839	camptothecin resistant clone CEM/C2 DNA topoisomerase I mRNA, partial	U07806.1	1	0.01%	1	0.01%
840	cdc14 homologue	AF000367	1	0.01%	1	0.01%
841	G1 to S phase transition 1 (GSPT1)	XM_055873.1	1	0.01%	1	0.01%
842	CASP8 associated protein 2 (RefSeq aa 2e-87)	NP_036247.1	1	0.01%	1	0.01%
843	programmed cell death 6 (PDCD6)	NM_013232.1	1	0.01%	1	0.01%
844	polymerase (DNA-directed) kappa (POLK), mRNA /cds=(172,2784) /gb=NM	Hs.135756	1	0.01%	1	0.01%
845	replication protein A2 (32kD)(RPA2)	NM_002946.1	1	0.01%	1	0.01%
846	tumor necrosis factor receptor	M58286	1	0.01%	1	0.01%
847	tumor suppressor protein (101F6), putative	AF040704	1	0.01%	1	0.01%
848	integral type I protein	NM_007364.1	1	0.01%	1	0.01%
849	musculus DnaJ-like protein 1 (Dnajl1)	NM_007869.1	1	0.01%	1	0.01%
850	BRI3	AF272043.1	1	0.01%	1	0.01%
851	novel protein (HSNOV1)	XM_017365.2	1	0.01%	1	0.01%
852	basic leucine zipper nuclear factor 1 (JEM-1) (BLZF1)	NM_003666.1	1	0.01%	1	0.01%
853	glycine cleavage system protein H (aminomethyl carrier) (RefSeq aa 2e-43	NP_004474.1	1	0.01%	1	0.01%
854	mitochondrial isoleucine tRNA synthetase, Length = 3367	D28500.1	1	0.01%	1	0.01%
855	LENG5 protein (LENG5), mRNA	NM_024075.1	1	0.01%	1	0.01%

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Figure 15 - Relative Est Frequency of Unique Known Genes Common to Mild and Severe cDNA Libraries - Page 1 of 19

Total ESTs from each library		12651	14222
Gene Name	Accession #	Mild OA	Severe OA
1 alpha gene sequence (=HSP90)	AF203815.1	580 4.58%	408 2.87%
2 fibronectin (FN)	X02761.1	198 1.57%	379 2.66%
3 collagen type III alpha 1 (COL3A1)	X08700	95 0.75%	337 2.37%
4 beta-2 microglobulin gene (B2M)	gb AF072097.1	200 1.58%	186 1.38%
5 mitochondrial genome (consensus sequence)	X62996	291 2.30%	194 1.36%
6 lumican (LUM)	NM_002345.1	116 0.92%	182 1.28%
7 collagen type I alpha 2 (COL1A2)	NM_000089.1	32 0.25%	176 1.24%
8 thymosin beta-4 (TMSB4X)	M17733	95 0.75%	156 1.10%
9 decorin (DCN)	NM_001920.1	234 1.85%	154 1.08%
10 osteoblast specific factor 2 (OSF-2os)	D13866.1	1 0.01%	123 0.86%
11 vimentin gene (VIM)	Z19554	46 0.36%	102 0.72%
12 mitochondrion, complete genome (=AF382012.1 haplotype M*1 mitochondrion)	NC_001807.2	114 0.90%	92 0.65%
13 elongation factor 1 alpha 1 (EEF1A1)	NM_001402.1	36 0.28%	89 0.63%
14 matrix Gla protein (MGP)	X53331	97 0.77%	80 0.56%
15 ribosomal protein S27 (=metalloproteinase 1 MPS1)	NM_001030.1	36 0.28%	70 0.49%
16 serine protease=HTRA serine protease (PRSS11)=AF157623.1	Y07921	32 0.25%	57 0.40%
17 ribosomal protein L7	X52967	63 0.50%	54 0.38%
18 proteoglycan 4 (=megakaryocyte stimulating factor)	AAB09089.1	287 2.27%	51 0.36%
19 scrapie responsive protein 1 (SCRG1)	NM_007281.1	56 0.44%	50 0.35%
20 transforming growth factor beta-induced, 68kD (TGFB1)	NM_000358.1	3 0.02%	47 0.33%
21 calmodulin 1 (phosphorylase kinase, delta) (CALM1)	NM_006888.1	31 0.25%	46 0.32%
22 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4 (9kD, MLR)	NM_002489.1	14 0.11%	46 0.32%
23 cytochrome c oxidase subunit VIc (COX6C)	NM_004374.1	22 0.17%	44 0.31%
24 Ribosomal protein S20 (RPS20)	NM_001023.1	23 0.18%	42 0.30%
25 osteonectin gene (SPARC) secreted protein, acidic, cysteine-rich	M25746.1	15 0.12%	42 0.30%
26 tumor protein translationally-controlled 1 (TPT1)	NM_003295.1	26 0.21%	37 0.26%
27 hexabrachion (tenascin C, cytactin) (HXB)	NM_002160.1	7 0.06%	37 0.26%
28 ribosomal protein L34 (RPL34)	NM_000995.1	22 0.17%	36 0.25%
29 thioredoxin (TXN)	J04026	22 0.17%	36 0.25%
30 asporin (ASPN) (LRR class 1)	NM_017680.1	24 0.19%	35 0.25%
31 annexin A2 (ANXA2) (lipocortin II)	NM_004039.1	7 0.06%	34 0.24%
32 transmembrane protein BRI	AF246221.1	37 0.29%	33 0.23%
33 ferritin heavy chain	L20841.1	7 0.06%	33 0.23%
34 ribosomal protein S25 (RPS25)	NM_001028.1	17 0.13%	32 0.23%
35 connective tissue growth factor (CTGF)	U14750	44 0.35%	31 0.22%
36 ribosomal protein L9	U06953	12 0.09%	30 0.21%
37 small nuclear ribonucleoprotein polypeptide G (SNRPG)	X85373	7 0.06%	29 0.20%
38 ribosomal protein S3a	M77234	18 0.14%	28 0.20%
39 translationally controlled tumor protein (TCTP)	X16064	17 0.13%	28 0.20%
40 RIBOSOMAL PROTEIN L17	spP18621	10 0.08%	27 0.19%
41 ribosomal protein L21	U14967.1	14 0.11%	26 0.18%
42 ribosomal protein L31	NM_000993.1	13 0.10%	25 0.18%
43 mimecan (OGN) (OIF)	AF202167.1	19 0.15%	24 0.17%
44 annexin I (lipocortin I) (ANX1) =X06908 (ORF)	NM_000700.1	11 0.09%	24 0.17%
45 putative p150	AAC51271.1	20 0.16%	22 0.15%
46 deleted in split hand/split foot 1 (DSS1)	U41515	11 0.09%	22 0.15%
47 mitochondrial ATPase coupling factor 6 subunit (ATP5A)	M37104	6 0.05%	22 0.15%
48 collagen type VI alpha 3 (COL6A3)	NM_004389.1	5 0.04%	22 0.15%
49 ribosomal protein S13	NM_001017.1	8 0.06%	21 0.15%

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Figure 15 - Relative Est Frequency of Unique Known Genes Common to Mild and Severe cDNA Libraries - Page 2 of 19

50	ribosomal RNA 18S	X03205	24	0.19%	20	0.14%
51	ribosomal protein L41	AF028844.1	14	0.11%	20	0.14%
52	cytochrome c oxidase subunit VIIb	Z14244	12	0.09%	20	0.14%
53	ribosomal protein S11 (RPS11)	NM_001015.1	11	0.09%	19	0.13%
54	ribosomal protein L27 (RPL27)	NM_000988.1	7	0.06%	19	0.13%
55	vitamin A responsive cytoskeleton related (JWA)	NM_006407.2	18	0.14%	18	0.13%
56	nascent-polypeptide-associated complex alpha polypeptide (NACA)	NM_005594.1	13	0.10%	18	0.13%
57	HSPC036 protein (=AF077200.1 HSPC014)	AF125097.1	8	0.06%	18	0.13%
58	CGI-134 protein (LOC51023)	NM_016067.1	4	0.03%	18	0.13%
59	ribosomal protein S6	M20020	13	0.10%	17	0.12%
60	ribosomal protein S29	L31610.1	8	0.06%	17	0.12%
61	androgen receptor associated protein 24 (ARA24) (=AF054183 GTP bi	AF052578	7	0.06%	17	0.12%
62	eukaryotic translation initiation factor 4 gamma, 2 (EIF4G2)	NM_001418.1	4	0.03%	17	0.12%
63	Sec81 gamma	AF054184	3	0.02%	17	0.12%
64	ribosomal protein L37	L11567	6	0.05%	16	0.11%
65	integrin beta 1 subunit	X07979.1	6	0.05%	16	0.11%
66	myosin regulatory light chain	X54304	4	0.03%	16	0.11%
67	gap junction protein, alpha 1, 43kD (connexin 43) (GJA1)	NM_000165.2	1	0.01%	16	0.11%
68	ribosomal DNA complete repeating unit	U13369.1	28	0.22%	15	0.11%
69	tumor rejection antigen (gp96) 1 (TRA1)	X15187	19	0.15%	15	0.11%
70	lysosome-associated protein, transmembrane - 4alpha (=D14696.1 Hur	U34259.1	10	0.08%	15	0.11%
71	cytochrome c oxidase, liver specific (EC 1.9.3.1.)	X15822	10	0.08%	15	0.11%
72	prothymosin alpha	M14630	9	0.07%	15	0.11%
73	F1-ATPase epsilon-subunit (ATP5E)	AF052955.1	7	0.06%	15	0.11%
74	cartilage intermediate layer protein, CILP	AB022430.1	17	0.13%	14	0.10%
75	ribosomal protein L6	X69391	11	0.09%	14	0.10%
76	S100 calcium-binding protein A4 (calcium protein, calvasculin, metast	gi4506764	11	0.09%	14	0.10%
77	ribosomal protein L38	Z26876	7	0.06%	14	0.10%
78	ribosomal protein L35a	NM_000996.1	3	0.02%	14	0.10%
79	H4 histone family, member G (H4FG)	NM_003542.2	3	0.02%	14	0.10%
80	KIAA0005	D13630	19	0.15%	13	0.09%
81	ribosomal protein L26	X69392	11	0.09%	13	0.09%
82	ribosomal protein S24	M31520	10	0.08%	13	0.09%
83	ribosomal protein L44 (RPL44)	NM_001001.1	10	0.08%	13	0.09%
84	collagen lysyl hydroxylase isoform 2 (PLOD2)	U84573	8	0.06%	13	0.09%
85	RIBOSOMAL PROTEIN L10 (QM PROTEIN) (TUMOR SUPPRESSOR C	spP27635	6	0.05%	13	0.09%
86	ribosomal protein L30	L05095.1	6	0.05%	13	0.09%
87	hH3.3B gene for histone H3.3	Z48950.1	6	0.05%	13	0.09%
88	ribosomal protein L39	D79205	4	0.03%	13	0.09%
89	calpactin 1 light chain	M81457	3	0.02%	13	0.09%
90	ribosomal protein L23a	U43701	13	0.10%	12	0.08%
91	Ribosomal protein L36 (=RPL44)	AF077043.1	10	0.08%	12	0.08%
92	cysteine dioxygenase	D85777	10	0.08%	12	0.08%
93	ribosomal protein L13	AF112214	8	0.05%	12	0.08%
94	endozepine (putative ligand of benzodiazepine receptor)	M15887.1	6	0.05%	12	0.08%
95	Ribosomal protein L4	NM_000968.1	4	0.03%	12	0.08%
96	heparan sulfate proteoglycan (HSPG) (OCI5)	J04621.1	4	0.03%	12	0.08%
97	pp21 homolog	AF125535.1	4	0.03%	12	0.08%
98	ribosomal protein S8 (RPS8)	NM_001012.1	3	0.02%	12	0.08%
99	calmodulin 2 (phosphorylase kinase, delta) (CALM2)	NM_001743.1	25	0.20%	11	0.08%
100	fibromodulin (FMOD)	NM_002023.2	19	0.15%	11	0.08%
101	caveolin 1 (CAV1)	AF125348.1	11	0.09%	11	0.08%

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Figure 15 - Relative Est Frequency of Unique Known Genes Common to Mild and Severe cDNA Libraries - Page 3 of 19

102	ribosomal protein L37a	L22154	8	0.06%	11	0.08%
103	ribosomal protein, large, P0 (RPLP0)	NM_001002.1	6	0.05%	11	0.08%
104	osteomodulin (OMD)	AB000114	6	0.05%	11	0.08%
105	lactate dehydrogenase A (LDHA)	NM_005568.1	5	0.04%	11	0.08%
106	dynein light chain 1 (hdic1), cytoplasmic	U32944	4	0.03%	11	0.08%
107	fibrillin (FBN1)	X63556	3	0.02%	11	0.08%
108	caldesmon	M64110	3	0.02%	11	0.08%
109	PRO2003	AF116679.1	2	0.02%	11	0.08%
110	ribosomal protein S7	M77233	2	0.02%	11	0.08%
111	ring-box 1 (RBX1)	NM_014248.1	2	0.02%	11	0.08%
112	HSPC005 (=C11orf10)	AF070661	1	0.01%	11	0.08%
113	H factor 1 (complement) (HF1)	NM_000186.1	17	0.13%	10	0.07%
114	high mobility group-1 protein (HMG-1)	X12597	12	0.09%	10	0.07%
115	spermidine/spermine N1-acetyltransferase	Z14136	10	0.08%	10	0.07%
116	ribosomal protein L7a (surf 3) large subunit	M36072	8	0.06%	10	0.07%
117	ribosomal protein L3 (RPL3)	NM_000967.1	7	0.06%	10	0.07%
118	transcription elongation factor B (SII), polypeptide 1-like (TCEB1L)	NM_003197.2	7	0.06%	10	0.07%
119	78 kD glucose-regulated protein (GRP78) gene (=BiP protein)	M19645.1	6	0.05%	10	0.07%
120	RNA polymerase II elongation factor-like protein	Z47087	5	0.04%	10	0.07%
121	prefoldin 5 (PFDN5) (=D89667 c-myc binding protein)	NP_002615.1	4	0.03%	10	0.07%
122	ribosomal protein L12	L06505	3	0.02%	10	0.07%
123	S100 calcium-binding protein A10 (annexin II ligand, calpactin I, light p	NM_002968.1	3	0.02%	10	0.07%
124	heat shock factor binding protein 1 (HSPB1)	NM_001537.1	2	0.02%	10	0.07%
125	CD9 antigen (p24/CD9)	L08125	10	0.08%	9	0.06%
126	eukaryotic translation initiation factor 3 (EIF3S6) (=INT6)	NM_001568.1	8	0.06%	9	0.06%
127	COX17 (yeast) homolog, cytochrome c oxidase assembly protein (CO	NM_005694.1	8	0.06%	9	0.06%
128	osteoclastogenesis inhibitory factor	AB008822	8	0.06%	9	0.06%
129	clusterin (CLU) SP40,40 (=M63379 TRPM-2 protein)	NM_001831.1	7	0.06%	9	0.06%
130	epithelial membrane protein 1 (EMP1)	NM_001423.1	6	0.05%	9	0.06%
131	BiP protein	X87949	6	0.05%	9	0.06%
132	ATP synthase, H transporting, mitochondrial F0 complex, subunit e (Re	NP_009031.1	4	0.03%	9	0.06%
133	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation pr	NM_003404.1	4	0.03%	9	0.06%
134	ribosomal protein L19	X63527	3	0.02%	9	0.06%
135	matrilin-3 (MATR3)	Y13341	3	0.02%	9	0.06%
136	Tubulin alpha isoform 1	AF081484	2	0.02%	9	0.06%
137	cytochrome c oxidase subunit VIIa (COX7A) muscle isoform	M83186	2	0.02%	9	0.06%
138	ribosomal protein L23	NM_000978.1	1	0.01%	9	0.06%
139	poly(A)-binding protein (PABP)	U68105	1	0.01%	9	0.06%
140	ribosomal protein S4, X-linked (RPS4X)	NM_001007.1	12	0.09%	8	0.06%
141	TSC-22 protein	U35048	12	0.09%	8	0.06%
142	HSPC312 (ORF) = AF161428.1 (=HSPC310)	AF161430	10	0.08%	8	0.06%
143	collagen type XI alpha 1 (COL11A1)	NM_001854.1	7	0.06%	8	0.06%
144	defender against cell death 1 (DAD1)	NM_001344.1	5	0.04%	8	0.06%
145	neuroendocrine-specific protein C like (nocen) (NSP-CL) reticulon 4 (R	NM_007008.1	5	0.04%	8	0.06%
146	calcyclin (=M14300 growth factor-inducible 2A9 gene; U04815 protein	J02763	4	0.03%	8	0.06%
147	solute carrier family 25 (mitochondrial carrier, phosphate carrier), mem	NM_005888.1	4	0.03%	8	0.06%
148	myosin, light polypeptide, regulatory, non-sarcomeric (20kD) (MLCB), r	Hs.233936	4	0.03%	8	0.06%
149	tomoregulin	AB004064.1	4	0.03%	8	0.06%
150	NADH dehydrogenase	X81900	3	0.02%	8	0.06%
151	ATP synthase epsilon chain	AF077045.1	3	0.02%	8	0.06%
152	collagen type V alpha 2 (COL5A2)	M11718	2	0.02%	8	0.06%
153	TGF-beta1/R alpha	D50683	2	0.02%	8	0.06%

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Figure 15 - Relative Est Frequency of Unlque Known Genas Common to Mild and Severe cDNA Libraries - Page 4 of 19

154	thrombospondin 2 (THBS2)	L12350	1	0.01%	8	0.06%
155	ribosomal protein L11	L05092.1	16	0.13%	7	0.05%
156	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG (=putative p150)	spP08547	14	0.11%	7	0.05%
157	ribosomal protein L5	U76609	10	0.08%	7	0.05%
158	mitochondrial ubiquinone-binding protein	M26700	10	0.08%	7	0.05%
159	HSPC310 (=HSPC312)	AF161428.1	8	0.06%	7	0.05%
160	ATP synthase, H transporting, mitochondrial F1F0, subunit g (ATP5JG)	NM_006476.1	7	0.06%	7	0.05%
161	cytochrome c oxidase subunit VIc (COX7C)	NM_001867.1	7	0.06%	7	0.05%
162	epididymal secretory protein (19.5kD) (HE1)	gi5453677	6	0.05%	7	0.05%
163	ribosomal protein S17	M13932	5	0.04%	7	0.05%
164	cytochrome b (ORF)	U09500	5	0.04%	7	0.05%
165	UMP-CMP kinase	AF110643.1	5	0.04%	7	0.05%
166	nucleolar phosphoprotein B23 (NPM1)	M28699	4	0.03%	7	0.05%
167	cartilage-derived C-type lectin (CLECSF1)	AF077345	4	0.03%	7	0.05%
168	histone H3.3	Z48950	4	0.03%	7	0.05%
169	ATP synthase, H transporting, mitochondrial F0 complex, subunit g (A)	Hs.107476	4	0.03%	7	0.05%
170	MORF-related gene X (KIAA0026) (=MRG15)	NM_012286.1	4	0.03%	7	0.05%
171	ATP synthase, H transporting, mitochondrial F1 complex, gamma poly	NM_005174.1	4	0.03%	7	0.05%
172	ATP synthase, H transporting, mitochondrial F1 complex, alpha subun	NM_004046.1	4	0.03%	7	0.05%
173	HSPC163	AF161512	4	0.03%	7	0.05%
174	actin, gamma 1 (ACTG1)	NM_001614.1	3	0.02%	7	0.05%
175	ribosomal protein L22 (RPL22)	NM_000983.1	3	0.02%	7	0.05%
176	muscleblind (Drosophila)-like (MBNL) (=KIAA0428)	NM_021038.1	3	0.02%	7	0.05%
177	ADP-ribosylation factor 4 (ARF4)	AF104238.1	3	0.02%	7	0.05%
178	vacuolar sorting protein VPS29/PEP11 (LOC51699)	NM_016226.1	3	0.02%	7	0.05%
179	palladin (KIAA0992)= CGI-151	NM_016081.1	2	0.02%	7	0.05%
180	vacuolar H-ATPase subunit	AF038954	2	0.02%	7	0.05%
181	calnexin (CANX) integral membrane protein, calnexin, (IP90)	M94859	2	0.02%	7	0.05%
182	annexin A5 (ANXA5)(lipocortin-V)	NM_001154.2	1	0.01%	7	0.05%
183	phosphoglycerate mutase (PGAM-B)	J04173	1	0.01%	7	0.05%
184	tissue inhibitor of metalloproteinase 3 (Sorsby fundus dystrophy, pseud	NM_000362.1	15	0.12%	6	0.04%
185	reverse transCRiptase	D84391	12	0.09%	6	0.04%
186	decay-accelerating factor	M31516	7	0.06%	6	0.04%
187	ribosomal protein L32 (RPL32)	NM_000994.1	6	0.05%	6	0.04%
188	PRO1574 (mitochondrial proteolipid 68MP homolog (PLPM)	AF116639.1	5	0.04%	6	0.04%
189	heterogeneous nuclear ribonucleoprotein D-like (HNRPDL)	NM_005463.1	5	0.04%	6	0.04%
190	heterogeneous nuclear ribonucleoprotein D (hnRNP D) (52% aa)	D55671	5	0.04%	6	0.04%
191	phospholipase A2	M86400	5	0.04%	6	0.04%
192	procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase)	Hs.41270	4	0.03%	6	0.04%
193	Cu/Zn superoxide dismutase (SOD)	X02317	4	0.03%	6	0.04%
194	ribosomal protein S12	X53505	3	0.02%	6	0.04%
195	ribosomal protein S23 (RPS23) =D14530 (ORF)	NM_001025.1	3	0.02%	6	0.04%
196	cathepsin K (pseudodysostosis)(CTSK)	NM_000396.1	3	0.02%	6	0.04%
197	p40	AAC51268.1	3	0.02%	6	0.04%
198	integrin, beta 1(fibronectin receptor, beta polypeptide, antigen CD29 in	NM_002211.1	3	0.02%	6	0.04%
199	15 kDa selenoprotein (SEP15)	AF051894	3	0.02%	6	0.04%
200	Fn54	AF001533.2	3	0.02%	6	0.04%
201	ribosomal protein S15a	X84407	2	0.02%	6	0.04%
202	T-cell cyclophilin	Y00052	2	0.02%	6	0.04%
203	FK506 binding protein (Fkbp63)	AF090334	2	0.02%	6	0.04%
204	ATPase, H transporting, lysosomal (vacuolar proton pump) 9kD (ATP6	NM_003945.1	2	0.02%	6	0.04%
205	calumenin (Calu) (calumenin)	AF013759	2	0.02%	6	0.04%

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Figure 18 - Relative Est Frequency of Unique Known Genes Common to Mild and Severe cDNA Libraries - Page 5 of 19

206	cell division cycle 10 (homologous to CDC10 of <i>S. cerevisiae</i>) (CDC10)	NM_001788.1	2	0.02%	6	0.04%
207	cig18 (=D31887.1 KIAA0062)	AF026940.1	2	0.02%	6	0.04%
208	phosphoglycerate kinase 1 (PGK1) (ORF)	NM_000291.1	2	0.02%	6	0.04%
209	nuclease sensitive element binding protein 1 (NSEP1) = L28809.1 dbp	NM_004559.1	2	0.02%	8	0.04%
210	cathepsin B (CTSB)	L22569	2	0.02%	6	0.04%
211	CGI-110 protein	AF151868.1	2	0.02%	6	0.04%
212	HS1 protein (=YWHAQ)	X57347	2	0.02%	6	0.04%
213	cell cycle progression 8 protein (CPR8)(ORF)=AF011794	NM_004748.1	2	0.02%	6	0.04%
214	inositol polyphosphate 1-phosphatase gene (INPP1) (low match)	AF141324.1	2	0.02%	6	0.04%
215	ribosomal protein L24 (RPL24) (=ribosomal protein L30)	NM_000986.1	1	0.01%	6	0.04%
216	cyclin	M74091	1	0.01%	6	0.04%
217	NADH dehydrogenase subunit 2 (ND2)	AF014897.2	1	0.01%	6	0.04%
218	Down syndrome candidate region 1 (DSCR1)	NM_004414.2	1	0.01%	6	0.04%
219	NAP (nucleosome assembly protein)	M86667	1	0.01%	6	0.04%
220	MRG15 protein (MRG15)	AF100615.1	1	0.01%	6	0.04%
221	PRO2853	AF119905.1	10	0.08%	5	0.04%
222	RIBOSOMAL PROTEIN L10A (CSA-19)(RPL10A)	P53025	7	0.06%	5	0.04%
223	peptidylglycine alpha-amidating monooxygenase (PAM)	M37721	7	0.06%	5	0.04%
224	selenoprotein P (SEPP1)	Z11793	5	0.04%	5	0.04%
225	insulin-like growth factor binding protein 7 (IGFBP7)	4504618	5	0.04%	5	0.04%
226	growth arrest-specific 1 (GAS1)	NM_002048.1	5	0.04%	5	0.04%
227	extracellular matrix protein	AB011792	5	0.04%	5	0.04%
228	SOD-2 manganese superoxide dismutase	X65965	4	0.03%	5	0.04%
229	mitochondrial signal peptidase	AF081737	4	0.03%	5	0.04%
230	transmembrane glycoprotein (GPNMB)	X76534	4	0.03%	5	0.04%
231	transcription elongation factor A (SII), 1 (TCEA1)	NM_008756.1	4	0.03%	5	0.04%
232	HSPC297 (=HSPC030)	AF181415.1	4	0.03%	5	0.04%
233	cyclin I	D50310	3	0.02%	5	0.04%
234	mitochondrial proteolipid 68MP homolog (PLPM)	NM_004894.1	3	0.02%	5	0.04%
235	hepatitis B virus X interacting protein (XIP)	AF029890	3	0.02%	5	0.04%
236	activated RNA polymerase (PC4)	NM_006713.1	3	0.02%	5	0.04%
237	myosin light chain 3 non-muscle (MLC3nm)	M31212	3	0.02%	5	0.04%
238	heat shock protein 86 (HSP86)	M30626.1	3	0.02%	5	0.04%
239	PTD014	AF092135.1	3	0.02%	5	0.04%
240	polyubiquitin	E12605	2	0.02%	5	0.04%
241	B-cell translocation protein 1 (BTG1)	X61123	2	0.02%	5	0.04%
242	small nuclear ribonucleoprotein D2 polypeptide (16.5kD) (SNRPD2)	NM_004597.3	2	0.02%	5	0.04%
243	pre-mRNA splicing factor (SFRS3)	AF107405.1	2	0.02%	5	0.04%
244	cytochrome c oxidase subunit VIIa polypeptide 2 like (COX7A2L)	NM_004718.1	2	0.02%	5	0.04%
245	FRG1	L76159	2	0.02%	5	0.04%
246	ribosomal protein S16	M60854	1	0.01%	5	0.04%
247	NADH dehydrogenase subunit 4L (RefSeq aa 2e-45)	gi5835396	1	0.01%	5	0.04%
248	mannosidase, beta A, lysosomal (MANBA) gene, and ubiquitin-conjug	AF224669.1	1	0.01%	5	0.04%
249	CD164 antigen, elaiomucin (CD164)	NM_006016.1	1	0.01%	5	0.04%
250	ganglioside expression factor 2 (GEF-2)	NM_007285.1	1	0.01%	5	0.04%
251	factor H homologue	M65294.1	1	0.01%	5	0.04%
252	dihydropyrimidinase-like 3 (DPYSL3)	NM_001387.1	1	0.01%	5	0.04%
253	stromal cell derived factor receptor 1 (SDFR1)	NM_012428.1	1	0.01%	5	0.04%
254	Pop-2=Purkinje cell protein 2	S40022	1	0.01%	5	0.04%
255	IGSF4 gene	AB017563.1	1	0.01%	5	0.04%
256	collagen type II alpha 1 (COL2A1)	J00116.1	15	0.12%	4	0.03%
257	complement factor H (=M17517)	Y00716	15	0.12%	4	0.03%

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Figure 15 - Relative Est Frequency of Unique Known Genes Common to Mild and Severe cDNA Libraries - Page 6 of 19

258	MEN1 region clone epsilon/beta	AF001893.1	8	0.06%	4	0.03%
259	ubiquinol-cytochrome c reductase complex (7.2 kD); hypothetical prote	NP_037519.1	8	0.06%	4	0.03%
260	breast carcinoma amplified sequence 2 (BCAS2)	NM_005872.1	8	0.06%	4	0.03%
261	SUI1 isolog	AF083441.1	6	0.05%	4	0.03%
262	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5 (RNA helicase, 68kD	NM_004396.1	6	0.05%	4	0.03%
263	hypoxia-inducible factor 1 alpha (HIF-1 alpha)	U22431	6	0.05%	4	0.03%
264	KIAA0728	AB018271.1	6	0.05%	4	0.03%
265	heat shock 10kD protein 1 (chaperonin 10) (HSP61)	NM_002157.1	5	0.04%	4	0.03%
266	platelet-derived growth factor receptor alpha (PDGFRA)	M21574	5	0.04%	4	0.03%
267	Cik-associated RS cyclophilin CARS-Cyp	U40763	5	0.04%	4	0.03%
268	ribosomal protein L13a (RPL13A)	NM_012423.1	4	0.03%	4	0.03%
269	ribosomal protein L15	NM_002948.1	4	0.03%	4	0.03%
270	thyroid receptor interactor (TRIP7)	L40357	4	0.03%	4	0.03%
271	vesicle docking protein p115 (P115)	NM_003715.1	4	0.03%	4	0.03%
272	heat shock J2 protein (HSJ2)	AF075601.1	4	0.03%	4	0.03%
273	tumor necrosis factor-inducible (TSG-6)	M31165	4	0.03%	4	0.03%
274	ribosomal protein, large, P1 (RPLP1)	NM_001003.1	3	0.02%	4	0.03%
275	heterogeneous nuclear ribonucleoprotein A1 (HNRPA1)	NM_002136.1	3	0.02%	4	0.03%
276	lysosomal membrane glycoprotein CD63 (=M59907 ME491;X07982)	M58485	3	0.02%	4	0.03%
277	Cyr61 protein (CYR61)	AF031385	3	0.02%	4	0.03%
278	BCL2/adenovirus E1B 19kD-interacting protein 3 (BNIP3)	U15174	3	0.02%	4	0.03%
279	amyloid-beta protein (APP)	M33112.1	3	0.02%	4	0.03%
280	hereditary haemochromatosis region, histone 2A-like protein gene, her	U91328.1	3	0.02%	4	0.03%
281	SEC24 (S. cerevisiae) related gene family, member D (SEC24D), = AK	(NM_014822.1	3	0.02%	4	0.03%
282	annexin A4 (ANXA4)	NM_001153.2	3	0.02%	4	0.03%
283	semaphorin E	AB000220	3	0.02%	4	0.03%
284	single-stranded DNA-binding protein (SSBP), nuclear gene encoding r	NM_003143.1	3	0.02%	4	0.03%
285	5' nucleotidase (EC 3.1.3.5)	X55740	3	0.02%	4	0.03%
286	AgX-1 antigen	S73498	3	0.02%	4	0.03%
287	frizzled-related protein (FRZB)	NM_001463.1	2	0.02%	4	0.03%
288	alpha E-catenin (CTNNA1) gene	AF102803.1	2	0.02%	4	0.03%
289	zinc finger transcription factor GKLF	AF105036.1	2	0.02%	4	0.03%
290	KIAA1247	AB033073.1	2	0.02%	4	0.03%
291	Lsm3 protein	AJ238095.1	2	0.02%	4	0.03%
292	SET translocation (myeloid leukemia-associated) (SET) =M93651	NM_003011.1	2	0.02%	4	0.03%
293	arginine-rich nuclear protein	M74002	2	0.02%	4	0.03%
294	actin-related protein Arp3 (ARP3)(actin-related protein 3 yeast)homolog	AF006083.1	2	0.02%	4	0.03%
295	CYTOCHROME C OXIDASE POLYPEPTIDE I	P00395	2	0.02%	4	0.03%
296	PRO0530	AF111849.1	2	0.02%	4	0.03%
297	small acidic protein	U51678	2	0.02%	4	0.03%
298	ATP SYNTHASE E CHAIN, MITOCHONDRIAL	spP56385	2	0.02%	4	0.03%
299	lost on transformation LOT1 (=PLAGL1)	U72621.2	2	0.02%	4	0.03%
300	N2A3 (=DPYSL2) (=dihydropyrimidinase related protein-2)	U97105	2	0.02%	4	0.03%
301	HIC protein	AF054589	2	0.02%	4	0.03%
302	CGI-148 protein	AF151906	2	0.02%	4	0.03%
303	ribosomal protein S21 (RPS21)	L04483	1	0.01%	4	0.03%
304	TI-227H (=tomoregulin; mitochondrial)	D50525	1	0.01%	4	0.03%
305	glucocorticoid-induced GILZ	AF228339	1	0.01%	4	0.03%
306	heat shock 70kD protein 10 (HSC71) (HSPA10)	NM_006597.1	1	0.01%	4	0.03%
307	actin binding protein ABP620	AB029290.1	1	0.01%	4	0.03%
308	profilin II	L10678.1	1	0.01%	4	0.03%
309	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation pr	NM_006826.1	1	0.01%	4	0.03%

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Figure 16 - Relative Est Frequency of Unique Known Genes Common to Mild and Severe cDNA Libraries - Page 7 of 19

310	sphingolipid activator protein 1	J03015	1	0.01%	4	0.03%
311	prolyl 4-hydroxylase gene	U14608.1	1	0.01%	4	0.03%
312	prion protein (p27-30) (Creutzfeld-Jakob disease, Gerstmann-Strausler	NM_000311.1	1	0.01%	4	0.03%
313	interleukin 1 receptor, type I (IL1R1) = M27492.1	NM_000877.1	1	0.01%	4	0.03%
314	KIAA0663	AB014563	1	0.01%	4	0.03%
315	palmitoyl-protein thioesterase (PPT)	AF022211	1	0.01%	4	0.03%
316	N-acylsphingosine amidohydrolase (ASAH) (acid ceramidase)	NM_004315.1	1	0.01%	4	0.03%
317	biglycan BGN	U11686.1	1	0.01%	4	0.03%
318	KIAA0102	D14658	1	0.01%	4	0.03%
319	vascular cell adhesion molecule 1 (VCAM1)	M30257	1	0.01%	4	0.03%
320	signal recognition particle subunit 9 (SRP9)	U20998	1	0.01%	4	0.03%
321	somatic cytochrome c (HCS) gene	M22877.1	1	0.01%	4	0.03%
322	calpastatin	D50827	1	0.01%	4	0.03%
323	H-2K binding factor-2	D14041	1	0.01%	4	0.03%
324	nucleobindin 2 (NUCB2)(NEFA protein)	X76732	1	0.01%	4	0.03%
325	Rap1B	U07795	1	0.01%	4	0.03%
326	X (inactive)-specific transCRipt (XIST)	M97168	1	0.01%	4	0.03%
327	NADH-UBIQUINONE OXIDOREDUCTASE MLRQ SUBUNIT (COMPL	spO00483	1	0.01%	4	0.03%
328	XAGL protein	Y15906.1	1	0.01%	4	0.03%
329	KIAA1038	AB028961	1	0.01%	4	0.03%
330	Ku autoimmune antigen gene	J04977.1	9	0.07%	3	0.02%
331	hypoxia-inducible gene 1 (HIG1) (=HSPC010)	AF145385.1	8	0.06%	3	0.02%
332	Tigger1 transposable element	U49973.1	7	0.06%	3	0.02%
333	cytosolic selenium-dependent glutathione peroxidase (=L09159 RHOA	M83094	7	0.06%	3	0.02%
334	sterol carrier protein 2	S52450	6	0.05%	3	0.02%
335	ribosomal protein S3 (RPS3)	NM_001005.1	5	0.04%	3	0.02%
336	enhancer of rudimentary homologue	U66871	5	0.04%	3	0.02%
337	Heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor	NM_004501.1	5	0.04%	3	0.02%
338	epidermal growth factor receptor kinase substrate (Eps8)	U12535	5	0.04%	3	0.02%
339	protein disulfide isomerase-related protein (P5)= D49489	NM_005742.1	5	0.04%	3	0.02%
340	paired mesoderm homeo box 1 (PMX1)	gi5902023	5	0.04%	3	0.02%
341	actin, beta (ACTB)	NM_001101.2	4	0.03%	3	0.02%
342	guanine nucleotide binding protein (G protein), beta polypeptide 2-like	NM_006098.1	4	0.03%	3	0.02%
343	aggrecan (chondroitin sulfate proteoglycan 1, large aggregating proteo	U13613	4	0.03%	3	0.02%
344	trophoblast STAT utron	AF080092.1	4	0.03%	3	0.02%
345	testis enhanced gene transCRipt protein (TEGT)	AF033095	4	0.03%	3	0.02%
346	heterogeneous nuclear ribonucleoprotein K (HNRPK)	NM_002140.1	4	0.03%	3	0.02%
347	UDP-glucose dehydrogenase (UGDH)	AF061016	4	0.03%	3	0.02%
348	uridine diphosphoglucose pyrophosphorylase	U27460	4	0.03%	3	0.02%
349	kinesin 1 (kinesin receptor) (KTN1)(= KIAA0004)	NM_004988.1	4	0.03%	3	0.02%
350	GOLGI 4-TRANSMEMBRANE SPANNING TRANSPORTER MTP (KIA	spQ15012	4	0.03%	3	0.02%
351	neural precursor cell expressed, developmentally down-regulated 5 (NE	NM_004404.1	3	0.02%	3	0.02%
352	chloride intracellular channel 4 like (CLIC4L)	NM_013943.1	3	0.02%	3	0.02%
353	DEK oncogene (DNA binding) (DEK)	gi4503248	3	0.02%	3	0.02%
354	S164 (=AC004858 U1 small ribonucleoprotein 1SNRP homologue)	AF109907	3	0.02%	3	0.02%
355	malate dehydrogenase 1, NAD (soluble) (MDH1)	NM_005917.1	3	0.02%	3	0.02%
356	matrilin-2 precursor	U69263	3	0.02%	3	0.02%
357	Golgi autoantigen, golgin subfamily a, 4 (GOLGA4)	NM_002078.2	3	0.02%	3	0.02%
358	spectrin SH3 domain binding protein 1 (SSH3BP1)	NM_005470.1	3	0.02%	3	0.02%
359	GTP-binding protein Sara	AF092130.1	3	0.02%	3	0.02%
360	C2H2 zinc finger protein (ZNF189)	AF025772.1	3	0.02%	3	0.02%
361	SON protein	AF183606	3	0.02%	3	0.02%

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Figure 15 - Relative Est Frequency of Unique Known Genes Common to Mild and Severe cDNA Libraries - Page 8 of 19

362	ribosomal protein L14	D87735	2	0.02%	3	0.02%
363	collagen type XII alpha 1 (COL12A1)	U57362	2	0.02%	3	0.02%
364	protein tyrosine phosphatase (hR-PTPu)	X58288	2	0.02%	3	0.02%
365	titin (TTN) gene	CAA49245.1	2	0.02%	3	0.02%
366	16.7Kd protein	AF078845.1	2	0.02%	3	0.02%
367	KIAA0438	AB007898.1	2	0.02%	3	0.02%
368	PAPS synthetase-2 (PAPSS2)	AF074331.1	2	0.02%	3	0.02%
369	ataxia telangiectasia (ATM) gene	U82828.1	2	0.02%	3	0.02%
370	constitutive fragile region FRA3B	AF152363.1	2	0.02%	3	0.02%
371	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5 (13kD, B13)	NM_005000.1	2	0.02%	3	0.02%
372	small membrane protein 1 (SMP1)	AF081282	2	0.02%	3	0.02%
373	glutaredoxin	X76648.1	2	0.02%	3	0.02%
374	KIAA0569	AB011141	2	0.02%	3	0.02%
375	KIAA0942 protein (KIAA0942)	NM_015310.1	2	0.02%	3	0.02%
376	cullin 4A (CUL4A)	AF077188.1	2	0.02%	3	0.02%
377	voltage-dependent anion channel (VDAC1)	AF151097.1	2	0.02%	3	0.02%
378	exportin 1 (CRM1, yeast, homolog) (XPO1) (ORF) =D89729, CRM1 prot	NM_003400.1	2	0.02%	3	0.02%
379	progesterone membrane binding protein (PMBP)	5453915	2	0.02%	3	0.02%
380	HSPC204	AF151038.1	2	0.02%	3	0.02%
381	HSPC034 protein	AF100747.1	2	0.02%	3	0.02%
382	TATA element modulatory factor	L01042.1	2	0.02%	3	0.02%
383	CGI-121 protein (LOC51002)	NM_016058.1	2	0.02%	3	0.02%
384	actinin beta-A subunit (=cDNA FLJ11041 fis, clone PLACE1004405, d	X57580.1	2	0.02%	3	0.02%
385	ferritin L chain	M11147	1	0.01%	3	0.02%
386	guanine nucleotide binding protein (G protein), alpha stimulating activ	NM_000516.2	1	0.01%	3	0.02%
387	nicotinamide N-methyltransferase (NNMT)	U08021	1	0.01%	3	0.02%
388	protein C inhibitor [human, leukocytes, Genomic, 1402 nt, segment 5 o	S69366.1	1	0.01%	3	0.02%
389	transcription factor BTF 3	X74070	1	0.01%	3	0.02%
390	GAP-associated tyrosine phosphoprotein p62 (Sam68) (SAM68) (=p62	NM_006559.1	1	0.01%	3	0.02%
391	collagen type VI alpha 1 (COL6A1)	X15880	1	0.01%	3	0.02%
392	t-complex-associated-testis-expressed 1-like (TCTE1L)=U02556=RP3	NM_006520.1	1	0.01%	3	0.02%
393	NADH-ubiquinone oxidoreductase AGGG subunit precursor homolog	AF067168.1	1	0.01%	3	0.02%
394	ubiquitin gene	U49869	1	0.01%	3	0.02%
395	CYTOCHROME C OXIDASE POLYPEPTIDE II	spP00403	1	0.01%	3	0.02%
396	cisplatin resistance-associated overexpressed protein	AB034205.1	1	0.01%	3	0.02%
397	Arp2/3 protein complex subunit p16 (ARC16) =AF006088 (ORF)	NM_005717.1	1	0.01%	3	0.02%
398	Eukaryotic translation initiation factor 2, subunit 2 (beta, 38kD)(EIF2S2	NM_003908.1	1	0.01%	3	0.02%
399	p75NTR-associated cell death executor (NADE)	AF187084.1	1	0.01%	3	0.02%
400	GW128	AF107406	1	0.01%	3	0.02%
401	SLC11A3 Iron transporter	AF215636.1	1	0.01%	3	0.02%
402	tine-1 protein ORF2 (=p150)	B28096	1	0.01%	3	0.02%
403	esterase D	AF112219	1	0.01%	3	0.02%
404	inositol 1,4,5-triphosphate receptor, type 2 (ITPR2)	NM_002223.1	1	0.01%	3	0.02%
405	SPHAR gene for cyclin-related protein	X82554.1	1	0.01%	3	0.02%
406	mitochondrial 16S rRNA	Z70759	1	0.01%	3	0.02%
407	murine leukemia viral (bmi-1) oncogene homolog (BMI1)	NM_005180.1	1	0.01%	3	0.02%
408	S1R protein (S1R) (=CGI-119)	AF113127.1	1	0.01%	3	0.02%
409	basic helix-loop-helix domain containing, class B, 2 (BHLHB2), mRNA	Hs.171825	1	0.01%	3	0.02%
410	predicted osteoblast protein (GS3786), mRNA	NM_014888.1	1	0.01%	3	0.02%
411	frizzled (Drosophila) homolog 1 (FZD1)	NM_003505.1	1	0.01%	3	0.02%
412	Dif33 protein homolog	AF164794.1	1	0.01%	3	0.02%
413	KIAA0244 gene	D87685	1	0.01%	3	0.02%

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Figure 15 - Relative Est Frequency of Unique Known Genes Common to Mild and Severe cDNA Libraries - Page 9 of 19

414:PRO2751	AF119896.1	1	0.01%	3	0.02%
415:protein x 0001	AF117230	1	0.01%	3	0.02%
416: dihydrofolate reductase (DHFR)	NM_000791.2	1	0.01%	3	0.02%
417: sorting nexin 3 (SNX3)	AF034548	1	0.01%	3	0.02%
418: two-handed zinc finger protein ZEB	U19969	1	0.01%	3	0.02%
419: beta-COP	X82103	1	0.01%	3	0.02%
420: RAD23 (S. cerevisiae) homolog B (RAD23B)	NM_002874.1	1	0.01%	3	0.02%
421: oligodendrocyte myelin glycoprotein (OMG)	L05367	1	0.01%	3	0.02%
422: KIAA1073	AB028996.1	1	0.01%	3	0.02%
423: PTD011	AF078864	1	0.01%	3	0.02%
424: Arginine-rich protein (ARP)	NM_006010.1	1	0.01%	3	0.02%
425: cyclin G2	U47414	1	0.01%	3	0.02%
426: Hmob33 protein	Y14155.1	1	0.01%	3	0.02%
427: HSPC039 protein	AF125100.1	1	0.01%	3	0.02%
428: Nuclear antigen Sp100 (SP100)	NM_003113.1	1	0.01%	3	0.02%
429: cytochrome-c oxidase subunit VIIaL precursor (COX7AL)	AF134406.1	1	0.01%	3	0.02%
430: metalloproteinase inhibitor TIMP-2	AF127803.1	1	0.01%	3	0.02%
431: DNAJ domain-containing protein MCJ (MCJ)	AF126743.1	1	0.01%	3	0.02%
432: steroid dehydrogenase homolog	AF076850.1	1	0.01%	3	0.02%
433: KIAA0829	AB020636	1	0.01%	3	0.02%
434: tubulin beta	AF070561	6	0.05%	2	0.01%
435: ARP2/3 protein complex subunit p21 (ARC21=AF006086 (ORF)	NM_005719.1	6	0.05%	2	0.01%
436: NS1-binding protein (NS1-BP) (=AB020657 KIAA0850)	AJ012449	6	0.05%	2	0.01%
437: syndecan binding protein (syntenin) (SDCBP)(ORF) = AF000652.1	NM_005625.1	5	0.04%	2	0.01%
438: proline-rich protein with nuclear targeting signal (B4-2)	NM_006813.1	5	0.04%	2	0.01%
439: Nck-associated protein 1 (Nap1) (=AB011159 KIAA0587)	AB014509.1	5	0.04%	2	0.01%
440: CD63 antigen (melanoma 1 antigen) (CD63)	NM_001780.1	4	0.03%	2	0.01%
441: zinc finger protein 216 (ZNF216)	AF062072.1	4	0.03%	2	0.01%
442: sin3 associated polypeptide (SAP18)	AF153608	4	0.03%	2	0.01%
443: sema domain immunoglobulin domain (Ig)(semaphorin) 3E (SEMA3E)	NM_012431.1	4	0.03%	2	0.01%
444: HepG2	D17039	4	0.03%	2	0.01%
445: RGC32 protein (RGC32)	NM_014059.1	4	0.03%	2	0.01%
446: UDP-glucose pyrophosphorylase 2 (ORF)	NM_006759.1	4	0.03%	2	0.01%
447: HSPC238	AF151072.1	4	0.03%	2	0.01%
448: polyposis locus (DP1 gene)	M73547	4	0.03%	2	0.01%
449: proteasome (prosome, macRopain) subunit, beta type, 1 (PSMB1)	NM_002793.1	4	0.03%	2	0.01%
450: cytoskeletal gamma-actin	X04098	3	0.02%	2	0.01%
451: elongation factor 1 beta 2 (EEF1B2)	NM_001959.1	3	0.02%	2	0.01%
452: NADH dehydrogenase(ubiquinone) Fe-S protein 5 (15kD) (NADH-coen	NM_004552.1	3	0.02%	2	0.01%
453: hairy (Drosophila)-homolog (HRY)	NM_005524.2	3	0.02%	2	0.01%
454: HSPC035 protein (LOC51669), NPD003	NM_016127.1	3	0.02%	2	0.01%
455: KIAA0970	AB023187.1	3	0.02%	2	0.01%
456: KIAA0332	AB002330	3	0.02%	2	0.01%
457: PTD010	AF078863.1	3	0.02%	2	0.01%
458: glyoxalase-I (GLO1)	AF146851.1	3	0.02%	2	0.01%
459: ras-related GTP-binding protein	AF106881.1	3	0.02%	2	0.01%
460: non-histone chromosomal protein (HMG-1)	L08048.1	3	0.02%	2	0.01%
461: SON DNA binding protein (SON)	X63753	3	0.02%	2	0.01%
462: N-terminal acetyltransferase complex ard1 subunit	AF085355.1	3	0.02%	2	0.01%
463: CMP-N-acetylneuraminic acid hydroxylase	AF074480.1	3	0.02%	2	0.01%
464: KIAA1250	AB033076.1	3	0.02%	2	0.01%
465: 5-aminimidazole-4-carboxamide ribonucleotide	NM_004044.1	3	0.02%	2	0.01%

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Figure 10- Relative Est Frequency of Unique Known Genes Common to Mild and Severe cDNA Libraries - Page 10 of 19

466	adenylyl cyclase-associated protein (CAP)	L12168	3	0.02%	2	0.01%
467	enterocyte differentiation associated factor EDAF-1	U62136.2	3	0.02%	2	0.01%
468	E6-AP ubiquitin-protein ligase (UBE3A)	AF009341.1	3	0.02%	2	0.01%
469	AKAP450 protein	AJ131693.1	3	0.02%	2	0.01%
470	protein-L-isoaspartate (D-aspartate) O-methyltransferase (PCMT1) (O	NM_005389.1	3	0.02%	2	0.01%
471	ribosomal protein, large P2 (RPLP2)	NM_001004.1	2	0.02%	2	0.01%
472	metallothionein-Ie (hMT-Ie)	M10942	2	0.02%	2	0.01%
473	thymosin beta-10	S54005	2	0.02%	2	0.01%
474	ubiquitin-conjugating enzyme E2B (RAD6 homolog) (UBE2B)	NM_003337.1	2	0.02%	2	0.01%
475	SMT3 (suppressor of mif two 3, yeast) homolog 2 (SMT3H2)	NM_006937.1	2	0.02%	2	0.01%
476	AD-017 protein	AF157318.1	2	0.02%	2	0.01%
477	KIAA0164	D79986	2	0.02%	2	0.01%
478	KIAA1077	AB029000.1	2	0.02%	2	0.01%
479	trichorhinophalangeal syndrome I gene (TRPS1)	NM_014112.1	2	0.02%	2	0.01%
480	TATA box binding protein (TBP)-associated factor, RNA polymerase II	NM_005642.1	2	0.02%	2	0.01%
481	SWI/SNF related, matrix associated (SMARCA1)	gi4507066	2	0.02%	2	0.01%
482	karyopherin alpha 4 (=importin alpha 3) (KPNA4)	NM_002268.1	2	0.02%	2	0.01%
483	apoptosis related protein APR-1	AF143235.2	2	0.02%	2	0.01%
484	sorting nexin 6 (SNX6)	AF121856.1	2	0.02%	2	0.01%
485	progesterone binding protein (HPR6.6)	gi5729874	2	0.02%	2	0.01%
486	proteasome subunit HC9	D00763	2	0.02%	2	0.01%
487	dermatopontin	Z22865	2	0.02%	2	0.01%
488	KIAA0766	AB018309.1	2	0.02%	2	0.01%
489	Id-2H	D13891	2	0.02%	2	0.01%
490	CGI-07 protein	AF132941.1	2	0.02%	2	0.01%
491	DNA polymerase zeta catalytic subunit (REV3)	AF157476.1	2	0.02%	2	0.01%
492	KIAA0382	AB002380	2	0.02%	2	0.01%
493	KIAA1053	AB028976.1	2	0.02%	2	0.01%
494	NY-REN-45 antigen (LOC51133)	NM_016121.1	2	0.02%	2	0.01%
495	splicing factor (CC1.4)	L10911.1	2	0.02%	2	0.01%
496	t-complex polypeptide 1	X52882	2	0.02%	2	0.01%
497	restin (Reed-Steinberg cell-expressed intermediate filament-associated	NM_002956.1	2	0.02%	2	0.01%
498	mannose 6-phosphate receptor, 46 kD (MPR46)	X56257	2	0.02%	2	0.01%
499	replication protein A3 (14kD) (RPA3)	NM_002947.1	2	0.02%	2	0.01%
500	anaphase promoting complex subunit 10	AF132794.1	2	0.02%	2	0.01%
501	KIAA0729	AB018272.1	2	0.02%	2	0.01%
502	lysophospholipase I (LYPLA1)	NM_006330.1	2	0.02%	2	0.01%
503	cofilin isoform 1	AF134802	2	0.02%	2	0.01%
504	HSPC213 (=HSPC327)	AAF36133.1	2	0.02%	2	0.01%
505	sperm antigen-36	AF187554.1	2	0.02%	2	0.01%
506	epb72	X85117	2	0.02%	2	0.01%
507	ribosomal protein L27A	AB020236.1	1	0.01%	2	0.01%
508	ubiquitin A-52 residue ribosomal protein fusion product 1 (UBA52)	gi4507760	1	0.01%	2	0.01%
509	enolase 1 (alpha) (ENO1)	NM_001428.1	1	0.01%	2	0.01%
510	dolichyl-phosphate beta-glucosyltransferase (ALG5)	AF102850.1	1	0.01%	2	0.01%
511	glutamine synthetase	S70290	1	0.01%	2	0.01%
512	syntrophin 4 binding protein UNC-18c (UNC-18c)	AF032922.1	1	0.01%	2	0.01%
513	lactate dehydrogenase B (LDH-B)	Y00711	1	0.01%	2	0.01%
514	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform (P	NM_002715.1	1	0.01%	2	0.01%
515	cellular growth-regulating protein	L10844	1	0.01%	2	0.01%
516	omithine aminotransferase	M29927	1	0.01%	2	0.01%
517	ORF2 contains a reverse transcriptase domain	AAA51622.1	1	0.01%	2	0.01%

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Figure 15 - Relative Est Frequency of Unique Known Genes Common to Mild and Severe cDNA Libraries - Page 11 of 19

518	ORF2 contains a reverse transcriptase domain	AAB59368.1	1	0.01%	2	0.01%
519	transforming, acidic coiled-coil containing protein 1 (TACC1=AF049910)	NM_006283.1	1	0.01%	2	0.01%
520	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor	NM_006854.2	1	0.01%	2	0.01%
521	poly(rC)-binding protein 1 (PCBP1)	NM_006196.1	1	0.01%	2	0.01%
522	Ia-associated invariant gamma-chain gene	M13560	1	0.01%	2	0.01%
523	uncharacterized bone marrow protein BM034 (=AK000571 FLJ20564)	AF217511.1	1	0.01%	2	0.01%
524	zinc finger protein SLUG (SLUG) gene	AF084243.1	1	0.01%	2	0.01%
525	basic transcription factor 2 p44 (btf2p44) gene, partial cds, neuronal	U80017.1	1	0.01%	2	0.01%
526	homeobox protein CDX4 (CDX4) gene	AF003530.1	1	0.01%	2	0.01%
527	KIAA0530	AB011102	1	0.01%	2	0.01%
528	ribosomal protein L33-like protein	AF047440	1	0.01%	2	0.01%
529	SOX4	AF124147.1	1	0.01%	2	0.01%
530	growth arrest specific transcription factor 5 gene	AF141346.1	1	0.01%	2	0.01%
531	protein phosphatase 1 catalytic subunit, beta isoform (PPP1CB)	NM_002709.1	1	0.01%	2	0.01%
532	glutaminase C	AF158555.1	1	0.01%	2	0.01%
533	DNA-binding protein A gene	L29073.1	1	0.01%	2	0.01%
534	YME1 (Saccharomyces-like 1 (YME1L1), = AJ132637.1 ATP-dependent m	NM_014263.1	1	0.01%	2	0.01%
535	LIM and SH3 protein 1 (LASP1) (=X82456 MLN50)	gi5453709	1	0.01%	2	0.01%
536	high mobility group 2 protein (HMG-2)	M83665	1	0.01%	2	0.01%
537	eukaryotic translation initiation factor 3, subunit 10 (theta, 150/170kD)	gi4503508	1	0.01%	2	0.01%
538	protein kinase C inhibitor-1	U27143	1	0.01%	2	0.01%
539	diphosphoinositol polyphosphate phosphohydrolase type 2 (NUDT4)	AF191654.2	1	0.01%	2	0.01%
540	copine III (CPNE3) (=AB014536 KIAA0636)	gi4503014	1	0.01%	2	0.01%
541	KIAA0077 gene	D38521.1	1	0.01%	2	0.01%
542	KIAA0680 gene product (KIAA0680)	NM_014721.1	1	0.01%	2	0.01%
543	KIAA1013	AB023230.1	1	0.01%	2	0.01%
544	secreta protein of unknown function (SPUF)	AF173937.1	1	0.01%	2	0.01%
545	CYTCHROME C OXIDASE POLYPEPTIDE III	P00414	1	0.01%	2	0.01%
546	farnesyl-protein transferase alpha-subunit	L00634	1	0.01%	2	0.01%
547	sequestosome 1 (SQSTM1) (=U46751.1 phosphotyrosine independent	NM_003900.1	1	0.01%	2	0.01%
548	Splicing factor proline/glutamine rich (polypyrimidine tract-binding prote	NM_005066.1	1	0.01%	2	0.01%
549	activin A receptor, type I (ACVR1) =Z22534 ALK-2	NM_001105.1	1	0.01%	2	0.01%
550	M-phase phosphoprotein homologue	AF100742.1	1	0.01%	2	0.01%
551	KIAA0336 gene	NM_014635.1	1	0.01%	2	0.01%
552	CGI-130 protein	AF151888.1	1	0.01%	2	0.01%
553	KIAA1058 protein	AB028981.1	1	0.01%	2	0.01%
554	LIV-1 protein, estrogen regulated (LIV-1) (=U41060)	7106340	1	0.01%	2	0.01%
555	Rosenthal fiber protein (alpha-B-Crystallin)	M24906	1	0.01%	2	0.01%
556	BPTF mRNA for bromodomain PHD finger transcription factor	AB032251.1	1	0.01%	2	0.01%
557	alpha subunit of GsGTP binding protein (GSA)	X56009	1	0.01%	2	0.01%
558	proteasome (prosome, macropain) subunit, beta type, 3 (PSMB3)	NM_002795.1	1	0.01%	2	0.01%
559	heterogeneous nuclear protein similar to rat helix destabilizing protein	NM_005758.1	1	0.01%	2	0.01%
560	Golgi vesicular membrane trafficking protein p18 (BET1)	gi5031610	1	0.01%	2	0.01%
561	fukutin	AB038490.1	1	0.01%	2	0.01%
562	KIAA0276	D87466	1	0.01%	2	0.01%
563	promyelocytic leukemia cell	M11948	1	0.01%	2	0.01%
564	phosphoglucomutase 1 (PGM1)	M83088	1	0.01%	2	0.01%
565	nucleotide binding protein, estradiol-induced (E2IG3)	NM_014366.1	1	0.01%	2	0.01%
566	Lysyl tRNA Synthetase	D32053.1	1	0.01%	2	0.01%
567	TPRC (=X97124 papillary renal cell carcinoma (translocation-associated	X99720	1	0.01%	2	0.01%
568	nuclear matrix protein 55	U89867.1	1	0.01%	2	0.01%
569	RNA binding motif protein 3 (RBM3) (=U28686)	5803136	1	0.01%	2	0.01%

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570	CGI-34 protein	AF132868.1	1	0.01%	2	0.01%
571	mitogen-activated protein kinase 3 (MAP4K3)	4506376	1	0.01%	2	0.01%
572	calcium channel alpha1E subunit (CACNA1E) gene	AF223391.1	1	0.01%	2	0.01%
573	brain cellular apoptosis susceptibility protein (CSE1)	AF053641	1	0.01%	2	0.01%
574	vacuolar ATPase isoform VA68	AF113129.1	1	0.01%	2	0.01%
575	septin 2-like cell division control protein	AF146760.1	1	0.01%	2	0.01%
576	KIAA1265	AB033091	1	0.01%	2	0.01%
577	guanylate binding protein isoform II (GBP-2)	M55543	1	0.01%	2	0.01%
578	RING zinc finger protein (RZF)	AF037204	1	0.01%	2	0.01%
579	L-isopartyl/D-aspartyl protein carboxyl methyltransferase isozyme I	M93009	1	0.01%	2	0.01%
580	cytochrome succinate dehydrogenase, small subunit	AB026906.1	1	0.01%	2	0.01%
581	interleukin 13 receptor alpha 1 (IL13RA1)	NM_001560.1	1	0.01%	2	0.01%
582	15 kDa selenoprotein (SEP15), mRNA /cds=(4,492) /gb=NM_004261 /Hs.90606	Hs.90606	1	0.01%	2	0.01%
583	HSPC019	AF077205.1	1	0.01%	2	0.01%
584	KIAA0783	AB018326.1	1	0.01%	2	0.01%
585	NDPP-1 protein	D10727.1	1	0.01%	2	0.01%
586	Sid3177	AB024935.1	1	0.01%	2	0.01%
587	SON DNA binding protein isoform E (SON) mRNA, complete cds, alternative splicing	Hs.92909	1	0.01%	2	0.01%
588	split hand/foot deleted gene 1	NP_033195.1	1	0.01%	2	0.01%
589	MKP-1 like protein tyrosine phosphatase	AF038844	1	0.01%	2	0.01%
590	Gem GTPase (gem)	U10650	1	0.01%	2	0.01%
591	plasma cell membrane glycoprotein (PC-1)	M57736.1	1	0.01%	2	0.01%
592	acyl-CoA synthetase 4 (ACS4)	AF030555	1	0.01%	2	0.01%
593	NADH-ubiquinone oxidoreductase MNLL subunit	AF050638.1	1	0.01%	2	0.01%
594	leucine-rich repeat (LRR) protein (P37NB) 37 kDa	NM_005824.1	1	0.01%	2	0.01%
595	beta-migrating plasminogen activator inhibitor I	M14083	1	0.01%	2	0.01%
596	proteasome subunit X (=X95586 MB1)	D29011	1	0.01%	2	0.01%
597	FUSE binding protein 3 (FBP3)	U69127.1	1	0.01%	2	0.01%
598	transcriptional activation factor TAFII32 (=AF151895 CGI-137 protein)	U21858	1	0.01%	2	0.01%
599	CGI-114 protein (=DKFZp566E144)	AF151872.1	1	0.01%	2	0.01%
600	CGI-123 protein	AF151881.1	1	0.01%	2	0.01%
601	CGI-24 protein	AF132958.1	1	0.01%	2	0.01%
602	nuclear pore complex protein hnp153	Z25535	1	0.01%	2	0.01%
603	ras-related YPT1 protein (ORF)	P11476	1	0.01%	2	0.01%
604	Opa-interacting protein OIP2	AF025438	1	0.01%	2	0.01%
605	cartilage link protein (CRTL1)	U43328.1	31	0.25%	1	0.01%
606	fatty acid binding protein (adipocyte lipid-binding protein)	NM_001442.1	18	0.14%	1	0.01%
607	hemoglobin beta chain (HBB)	AF117710	16	0.13%	1	0.01%
608	fatty acid binding protein 4, adipocyte (FABP4), mRNA /cds=(47,445) /Hs.83213	Hs.83213	15	0.12%	1	0.01%
609	ubiquitin-like 1 (sentrin) (UBL1) (=SUMO-1)	NM_003352.1	9	0.07%	1	0.01%
610	phenylethylamine binding protein gene	AF198969.1	7	0.06%	1	0.01%
611	signal recognition particle 14kD (homologous Alu RNA-binding protein)	NM_003134.1	6	0.05%	1	0.01%
612	KVLQT1 gene (=p150)	AJ006345.1	6	0.05%	1	0.01%
613	alpha-2-macroglobulin	D83186	6	0.05%	1	0.01%
614	metallothionein 1L (MT1L)	NM_002450.1	5	0.04%	1	0.01%
615	thrombospondin 1 (THBS1)	NM_003246.1	5	0.04%	1	0.01%
616	Kallmann syndrome 1 (KAL1) (=ADMLX=putative adhesion molecule)	NM_000216.1	5	0.04%	1	0.01%
617	YAP65	X80507.1	4	0.03%	1	0.01%
618	protein phosphatase 2A catalytic subunit-beta	M60484	4	0.03%	1	0.01%
619	KIAA0191 (zinc finger homolog)	D83776	4	0.03%	1	0.01%
620	protein immuno-reactive with anti-PTH polyclonal antibodies	U28831.1	4	0.03%	1	0.01%
621	ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR	spP36542	4	0.03%	1	0.01%

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622	catalase	X04076	4	0.03%	1	0.01%
623	HSPC067	AF161552.1	4	0.03%	1	0.01%
624	ribosomal RNA 16S gene	AF036008.1	4	0.03%	1	0.01%
625	ribosomal protein L8	Z28407	3	0.02%	1	0.01%
626	peripheral myelin protein 22	M94048	3	0.02%	1	0.01%
627	dioxin-inducible cytochrome P450 (CYP1B1)	U03688.1	3	0.02%	1	0.01%
628	MAGUK protein p55T (=AB002323 KIAA0325)	AF162130.1	3	0.02%	1	0.01%
629	PPP1R5	AF110824.1	3	0.02%	1	0.01%
630	splicing factor SRp40-1 (SRp40)	U30826.1	3	0.02%	1	0.01%
631	splicing factor, arginine/serine-rich 5 (RefSeq aa 1e-54)	NP_008858.1	3	0.02%	1	0.01%
632	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1	spP03886	3	0.02%	1	0.01%
633	HSPC307	AF161425.1	3	0.02%	1	0.01%
634	immunoglobulin light chain	D87000	3	0.02%	1	0.01%
635	lysosomal-associated membrane glycoprotein-1 (LAMP1) (=J04182)	L08582	3	0.02%	1	0.01%
636	comichon protein	AF070654.1	3	0.02%	1	0.01%
637	okadaic acid-inducible and cAMP-regulated phosphoprotein 19 (ARPP)	AF084555.1	3	0.02%	1	0.01%
638	SH3 domain-containing protein SH3P18	U61167	3	0.02%	1	0.01%
639	KIAA1025	AB028948.1	3	0.02%	1	0.01%
640	LGMD2B	AJ007973	3	0.02%	1	0.01%
641	CAR (RFP2)	AF279660	3	0.02%	1	0.01%
642	NADH dehydrogenase(ubiquinone) 1 beta subcomplex, 3 (12kD, B12)	NM_002491.1	3	0.02%	1	0.01%
643	KIAA0579	AB011151.1	3	0.02%	1	0.01%
644	KIAA0977	AB023194.1	3	0.02%	1	0.01%
645	KIAA0573	AB011145	3	0.02%	1	0.01%
646	polyadenylate binding protein-interacting protein 1 (PAIP1)	NM_006451.1	3	0.02%	1	0.01%
647	Translocon associated protein gamma subunit	spQ9UNL2	3	0.02%	1	0.01%
648	secreted frizzled-related protein 4 (SFRP4)	NM_003014.2	3	0.02%	1	0.01%
649	phosphatase 1, catalytic subunit, gamma isoform (PPP1CC) mRNA	NM_002710.1	3	0.02%	1	0.01%
650	ring finger protein (C3H2C3 type) 6 (RNF6)	NM_005977.1	3	0.02%	1	0.01%
651	putative transmembrane protein E3-16	AF092128.1	3	0.02%	1	0.01%
652	epithelial protein lost in neoplasm beta (EPLIN)	NM_016357.1	3	0.02%	1	0.01%
653	laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1)(ORF)	NM_002295.1	2	0.02%	1	0.01%
654	t-complex-associated-testis-expressed 1-like 1 (TCTEL1)	NM_006519.1	2	0.02%	1	0.01%
655	collagen type XIV variant C-terminal NC1 and 3'UTR	Y11711	2	0.02%	1	0.01%
656	reverse transcriptase related protein	prf1207289A	2	0.02%	1	0.01%
657	JKTBP2, JKTBP1, complete cds	AB017018.1	2	0.02%	1	0.01%
658	latent transforming growth factor beta binding protein 1 (LTBP1)	NM_006627.1	2	0.02%	1	0.01%
659	laminin B2 chain	M55210	2	0.02%	1	0.01%
660	HSPC025 (HSPC025)	NM_016091.1	2	0.02%	1	0.01%
661	insulin-like growth factor I	X57025	2	0.02%	1	0.01%
662	clathrin, light polypeptide (Lca) (CLTA)	NM_007096.1	2	0.02%	1	0.01%
663	IDN3	AB019494.1	2	0.02%	1	0.01%
664	KIAA0069 gene	D31885.1	2	0.02%	1	0.01%
665	immunoglobulin lambda gene	D87003.1	2	0.02%	1	0.01%
666	KIAA0038 gene	D26068.1	2	0.02%	1	0.01%
667	disabled 2 p93 (DAB2) (mitogen-responsive phosphoprotein) (DAB2)	AF188298.1	2	0.02%	1	0.01%
668	CD36 antigen	L06850.1	2	0.02%	1	0.01%
669	guanine nucleotide binding protein 11 (GNG11) = U31384.1	NM_004126.1	2	0.02%	1	0.01%
670	KIAA0436	AB007896	2	0.02%	1	0.01%
671	conserved gene amplified in osteosarcoma (OS4)	NM_005730.1	2	0.02%	1	0.01%
672	mitochondrial coxII	X55654.1	2	0.02%	1	0.01%
673	cytochrome C oxidase II subunit (ORF)	X55654	2	0.02%	1	0.01%

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Figure 15 Relative Est Frequency of Unique Known Genes Common to Mild and Severe cDNA Libraries - Page 14 of 19

674	NADH-ubiquinone oxidoreductase subunit CI-B14	AF047182	2	0.02%	1	0.01%
675	mouse tropomyosin homolog (HSPC001) = AF047439(ORF)	NM_004872.1	2	0.02%	1	0.01%
676	heterogeneous nuclear ribonucleoprotein R (ORF)	AF000364	2	0.02%	1	0.01%
677	destin (actin depolymerizing factor) (ADF)	5802965	2	0.02%	1	0.01%
678	KIAA0127	NM_014755.1	2	0.02%	1	0.01%
679	KIAA0577	AB011149	2	0.02%	1	0.01%
680	PTH-responsive osteosarcoma D1 protein	AAD25980.1	2	0.02%	1	0.01%
681	Polyadenylate binding protein	U75688.1	2	0.02%	1	0.01%
682	lymphocyte activation-associated protein	AF123320.1	2	0.02%	1	0.01%
683	calcineurin A2	M29551	2	0.02%	1	0.01%
684	KIAA0610	AB011182	2	0.02%	1	0.01%
685	SRY (sex-determining region Y)-box 5 (SOX5)	NM_006940.1	2	0.02%	1	0.01%
686	glucan (1,4-alpha-), branching enzyme 1(ORF)(glycogen branching en	NM_000158.1	2	0.02%	1	0.01%
687	p58/GTA (galactosyltransferase associated protein kinase)	M37712.1	2	0.02%	1	0.01%
688	mesenchyme homeo box 2 (growth arrest-specific homeo box) (MEOX	NM_005924.1	2	0.02%	1	0.01%
689	proteasome (prosome, macropain) subunit, alpha type, 2 (PSMA2)	NM_002787.1	2	0.02%	1	0.01%
690	G protein-coupled receptor 84 (GPR84)	NM_005756.1	2	0.02%	1	0.01%
691	germline T-cell receptor beta chain	U66061	2	0.02%	1	0.01%
692	SH3 domain binding glutamic acid-rich protein like (SH3BGRL)	NM_003022.1	2	0.02%	1	0.01%
693	KIAA0256	D87445	2	0.02%	1	0.01%
694	KIAA1102	AB029025.1	2	0.02%	1	0.01%
695	KIAA1380 protein	AB037801.1	2	0.02%	1	0.01%
696	angiotensin-like 1 (ANGPTL1)	NM_004673.1	2	0.02%	1	0.01%
697	uncharacterized hypothalamus protein HARP11 (HARP11)	NM_018477.1	2	0.02%	1	0.01%
698	multiple PDZ domain protein (MPDZ) = AF093419.1	NM_003829.1	2	0.02%	1	0.01%
699	proto-oncogene tyrosine-protein kinase (ABL) gene	U07563.1	2	0.02%	1	0.01%
700	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1 (YES1)	NM_005433.1	2	0.02%	1	0.01%
701	inactive progesterone receptor, 23 kD (P23) = L24804.1= Q15185 (or	NM_006601.1	2	0.02%	1	0.01%
702	histone acetyltransferase 1	AF030424	2	0.02%	1	0.01%
703	small acidic protein (IMAGE145052)	NM_014267.1	2	0.02%	1	0.01%
704	CGI-99 protein = homeobox prox 1= AF100755.1(ORF)	AF151857	2	0.02%	1	0.01%
705	mSin3A (sin3A)	U22394	2	0.02%	1	0.01%
706	CG3450 gene product [Drosophila melanogaster](86% ORF)	AAF57398.1	2	0.02%	1	0.01%
707	ENDOPLASMIN PRECURSOR (94 KD GLUCOSE-REGULATED PRO	spP14825	2	0.02%	1	0.01%
708	gene hY3 encoding a cytoplasmic Ro RNA	V00585.1	2	0.02%	1	0.01%
709	HSPC004	AF070660	2	0.02%	1	0.01%
710	HSPC161	AF161510	2	0.02%	1	0.01%
711	KIAA0205	D86960	2	0.02%	1	0.01%
712	KIAA0238	D87075	2	0.02%	1	0.01%
713	KIAA0716	AB018259.1	2	0.02%	1	0.01%
714	SUMO-1 activating enzyme subunit 2 (UBA2)	NM_005499.1	2	0.02%	1	0.01%
715	TEB4 protein (=AB011169 KIAA0597)	AF009301	2	0.02%	1	0.01%
716	XIST	X56196	2	0.02%	1	0.01%
717	nCL1 gene	X85032.1	2	0.02%	1	0.01%
718	small nuclear ribonucleoprotein D1 polypeptide (16kD) (SNRPD1)	NM_006938.1	2	0.02%	1	0.01%
719	ALEX1 protein (LOC51309)	NM_016608.1	2	0.02%	1	0.01%
720	MHC class II lymphocyte antigen beta-chain (HLA-DPB1)	M28202.1	2	0.02%	1	0.01%
721	cAMP-dependent protein kinase subunit RII-beta	M31158	2	0.02%	1	0.01%
722	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue spec	NM_002734.1	2	0.02%	1	0.01%
723	rab11a GTPase	AF000231	2	0.02%	1	0.01%
724	rab3 GTPase-activating protein, non-catalytic subunit (150kD) (RAB3-C	NM_012414.1	2	0.02%	1	0.01%
725	Ca2-activated neutral protease large subunit (CANP)	M23254.1	2	0.02%	1	0.01%

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Figure 15- Relative Est Frequency of Unique Known Genes Common to Mild and Severe cDNA Libraries - Page 15 of 19

726	histone H2A.Z= M37583	X52317	2	0.02%	1	0.01%
727	inhibitor of apoptosis protein 2	U45879	2	0.02%	1	0.01%
728	KIAA0594	AB011166	2	0.02%	1	0.01%
729	ring finger protein 13 (RNF13), mRNA /cgs=(151,1296) /gb=NM_007262	Hs.6900	2	0.02%	1	0.01%
730	ribosomal protein S18	X69150.1	1	0.01%	1	0.01%
731	ribosomal protein S5 (RPS5)	NM_001009.1	1	0.01%	1	0.01%
732	metallothionein-II (mt-II)	J00271	1	0.01%	1	0.01%
733	v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS)	NM_005252.2	1	0.01%	1	0.01%
734	deiodinase, iodothyronine, type II (DIO2), transCRipt variant 1	gi7549802	1	0.01%	1	0.01%
735	insulin-like growth factor binding protein 5 (IGFBP5) gene	L27556.1	1	0.01%	1	0.01%
736	enhancer-of-split and hairy-related protein 1 (SHARP-1)	AF009329.1	1	0.01%	1	0.01%
737	colon carcinoma laminin-binding protein (=RIBOSOMAL PROTEIN SA)	J03799.1	1	0.01%	1	0.01%
738	transmembrane protein (p63)	X69910	1	0.01%	1	0.01%
739	peroxiredoxin 1 (PRDX1) (=NKEFA)	NM_002574.1	1	0.01%	1	0.01%
740	RIBOSOMAL PROTEIN SA (P40)	spP08865	1	0.01%	1	0.01%
741	WSB-1 isoform	AF106684.1	1	0.01%	1	0.01%
742	high-mobility group (nonhistone chromosomal) protein 17 (HMG17)	NM_005517.1	1	0.01%	1	0.01%
743	prostatic binding protein (PBP)	NM_002567.1	1	0.01%	1	0.01%
744	complement component 1, s subcomponent (C1S)	NM_001734.1	1	0.01%	1	0.01%
745	dual specificity phosphatase 1 (DUSP1)	NM_004417.2	1	0.01%	1	0.01%
746	KIAA0143 gene	D63477.1	1	0.01%	1	0.01%
747	non-metastatic cells 2, protein (NM23B) expressed in (NME2)	NM_002512.1	1	0.01%	1	0.01%
748	high density lipoprotein binding protein (HBP)	M64098	1	0.01%	1	0.01%
749	cathepsin L (CTSL)	NM_001912.1	1	0.01%	1	0.01%
750	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1 (7kD, MNLL)	NM_004545.1	1	0.01%	1	0.01%
751	cyclophilin-related protein (NKTR) gene (=PAC RPC14-613B23)	AF184110.1	1	0.01%	1	0.01%
752	U50HG genes for U50' snoRNA and U50 snoRNA, complete sequence	AB017710	1	0.01%	1	0.01%
753	RAD21 (S. pombe) homolog (RAD21) (=X98294)	gi5453993	1	0.01%	1	0.01%
754	myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) hom	NM_005935.1	1	0.01%	1	0.01%
755	chaperonin containing TCP1 subunit 4 (delta) (CCT4)	NM_006430.1	1	0.01%	1	0.01%
756	Membrane cofactor protein	X59408.1	1	0.01%	1	0.01%
757	KIAA0349 gene	AB002347.1	1	0.01%	1	0.01%
758	p130 (130K protein)	X76061.1	1	0.01%	1	0.01%
759	ORF2 (Canis familiaris)(60%)	AB012223	1	0.01%	1	0.01%
760	karyopherin (importin) beta 1 (KPMB1) (=L38951 importin beta subunit)	gi4504904	1	0.01%	1	0.01%
761	signal peptidase complex (18kD) (SPC18)	NM_014300.1	1	0.01%	1	0.01%
762	hexosaminidase B (beta polypeptide) (HEXB)(ORF)	NM_000521.1	1	0.01%	1	0.01%
763	four and a half LIM domains 1 (FHL1)	NM_001449.1	1	0.01%	1	0.01%
764	fibroblast growth factor 2 (basic)(FGF2)	NM_002006.1	1	0.01%	1	0.01%
765	NADH dehydrogenase(ubiquinone) 1, alpha/beta subcomplex, 1 (8kD,	NM_005003.1	1	0.01%	1	0.01%
766	5T4 oncofetal trophoblast glycoprotein (5T4)	NM_006670.1	1	0.01%	1	0.01%
767	Autosomal Highly Conserved Protein (AHCP) (=DKFZp586G051)	NM_016255.1	1	0.01%	1	0.01%
768	KIAA0853	AB020660.1	1	0.01%	1	0.01%
769	meningioma-expressed antigen 5 (MEA5) (=KIAA0679)	AF036145	1	0.01%	1	0.01%
770	PTEN (PTEN) gene	AF143312.1	1	0.01%	1	0.01%
771	prolylcarboxypeptidase (angiotensinase C) (PRCP)	NM_005040.1	1	0.01%	1	0.01%
772	GLI-Kruppel family member GLI3 (Greig cephalopolysyndactyly syndro	gi4504014	1	0.01%	1	0.01%
773	zinc finger protein 84 (HPF2) (ZNF84)	NM_003428.1	1	0.01%	1	0.01%
774	RNA polymerase II subunit hSRPB7	U20659.1	1	0.01%	1	0.01%
775	tubulin-specific chaperone a (TBCA) (=AF038952 cofactor A protein)	gi4759211	1	0.01%	1	0.01%
776	polycystic kidney disease 2 (autosomal dominant)	NM_000297.1	1	0.01%	1	0.01%
777	oxysterol-binding protein	AB017026	1	0.01%	1	0.01%

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Figure 15 - Relative Est Frequency of Unique Known Genes Common to Mild and Severe cDNA Libraries - Page 16 of 19

778	ubiquinol-cytochrome c reductase core protein II (UQCRC2)(ORF) = JQNM_003368.1	1	0.01%	1	0.01%	
779	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L	spP03901	1	0.01%	1	0.01%
780	thioredoxin peroxidase (antioxidant enzyme) (AOE372) =U25182(ORF)	NM_006406.1	1	0.01%	1	0.01%
781	cytoskeletal tropomyosin TM30(nm)	X04588.1	1	0.01%	1	0.01%
782	ring finger protein 4 (RNF4)	gi4506560	1	0.01%	1	0.01%
783	TSE1=protein kinase A regulatory subunit	S54711	1	0.01%	1	0.01%
784	SUMO-1-specific protease (KIAA0797)	NM_015571.1	1	0.01%	1	0.01%
785	myosin-binding protein C, cardiac (MYBPC3)	NM_000256.1	1	0.01%	1	0.01%
786	ATP synthase, H transporting, mitochondrial F0 complex, subunit f, iso	NM_004889.1	1	0.01%	1	0.01%
787	hect domain and RLD 2(HERC2) (=KIAA0393)	NM_004667.2	1	0.01%	1	0.01%
788	integrin cytoplasmic domain associated protein (Icap-1a)	AF012023	1	0.01%	1	0.01%
789	BUP	AF078848.1	1	0.01%	1	0.01%
790	KIAA0235	D87078	1	0.01%	1	0.01%
791	PDNP1 gene (nucleotide pyrophosphatase)	AF110304.1	1	0.01%	1	0.01%
792	phosphoribosyl pyrophosphate synthetase subunit I	D00860.1	1	0.01%	1	0.01%
793	wbsCR1 (WBSCR1)	AF045555.1	1	0.01%	1	0.01%
794	proteasome (prosome, macropain) subunit, alpha type, 3 (PSMA3)	NM_002788.1	1	0.01%	1	0.01%
795	CLP (CLPP)	L54057.1	1	0.01%	1	0.01%
796	Tax1 (human T-cell leukemia virus type I) binding protein 1 (TAX1BP1)	NM_006024.2	1	0.01%	1	0.01%
797	platelet-activating factor acetylhydrolase, isoform 1b, alpha subunit (PA	4557740	1	0.01%	1	0.01%
798	transferrin receptor (TFRC) gene	AF187320	1	0.01%	1	0.01%
799	CGI-127 protein	AF151885.1	1	0.01%	1	0.01%
800	microvascular endothelial differentiation gene 1 product	AB026908.1	1	0.01%	1	0.01%
801	vanilloid receptor, CARKL and CTNS; TIP1; P2X5b and P2X5a	AF168787.1	1	0.01%	1	0.01%
802	vitalgo-associated protein VIT-1 (VIT1) (=DKFZp564K2364)	AF264714.1	1	0.01%	1	0.01%
803	small EDRK-rich factor 1, long isoform (SERF1) (=bt12p44)	AF073519.1	1	0.01%	1	0.01%
804	translin	X78627	1	0.01%	1	0.01%
805	ionizing radiation resistance conferring protein (=X83544 DAP-3)	U18321	1	0.01%	1	0.01%
806	CGI-116 protein(LOC51019)(ORF)= AF155655 protein x 0009 mRNA	NM_016053.1	1	0.01%	1	0.01%
807	tropomyosin	M19267	1	0.01%	1	0.01%
808	hXBP-1 transcription factor DNA (=TREB protein)	L13850.1	1	0.01%	1	0.01%
809	KARP-1-binding protein 3 (=KIAA0470)	AB022659.1	1	0.01%	1	0.01%
810	inducible 6-phosphofructo-2-kinase/fructose 2,6-bisphosphatase (IPFK)	AF056320	1	0.01%	1	0.01%
811	GTPase activating protein (rap1GAP)	M64788	1	0.01%	1	0.01%
812	guanine nucleotide binding protein (G protein), alpha inhibiting activity	NM_006496.1	1	0.01%	1	0.01%
813	COX VIa-L cytochrome c oxidase liver-specific subunit VIa (EC 1.9.3.1)	X15341.1	1	0.01%	1	0.01%
814	integrin, beta 5 (ITGB5)	NM_002213.1	1	0.01%	1	0.01%
815	DNA topoisomerase II (TOP2)	Z15115	1	0.01%	1	0.01%
816	squalene epoxidase	D78129	1	0.01%	1	0.01%
817	Kruppel-related DNA-binding protein (PF4)	M61866	1	0.01%	1	0.01%
818	RNA helicase	AJ223948	1	0.01%	1	0.01%
819	nuclear receptor subfamily 3, group C, member 1 (NR3C1)	NM_000176.1	1	0.01%	1	0.01%
820	potassium channel modulatory factor (=DKFZp434L1021)	AF155652.1	1	0.01%	1	0.01%
821	nuclear phosphoprotein similar to S. cerevisiae	NM_007062.1	1	0.01%	1	0.01%
822	COP9 complex subunit 4 (LOC51138)	NM_016129.1	1	0.01%	1	0.01%
823	endomembrane protein EMP70 precursor isologue	U95973	1	0.01%	1	0.01%
824	adipocyte acid phosphatase beta=phenylarsine oxide-sensitive tyrosyl	S62885.1	1	0.01%	1	0.01%
825	dead box, X isoform (DBX)	AF000982.1	1	0.01%	1	0.01%
826	major histocompatibility locus class III regions Hsc70l (smRNP, G7A, N	AF109905	1	0.01%	1	0.01%
827	ankyrin G (ANK-3)	U13616.1	1	0.01%	1	0.01%
828	spectrin beta protein (pAZSP 3' end)	X91849.2	1	0.01%	1	0.01%
829	antigen NY-CO-1 (NY-CO-1)	AF039687.1	1	0.01%	1	0.01%

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Figure 15 - Relative Est Frequency of Unique Known Genes Common to Mild and Severe cDNA Libraries - Page 17 of 19

830	GS3955	D87119	1	0.01%	1	0.01%
831	HBV pX associated protein-8 (LOC51773)	NM_016578.1	1	0.01%	1	0.01%
832	hyperion gene	AJ010770	1	0.01%	1	0.01%
833	KIAA0090	D42044	1	0.01%	1	0.01%
834	KIAA0170	D79992	1	0.01%	1	0.01%
835	KIAA0379	AB002377	1	0.01%	1	0.01%
836	myeloid cell nuclear differentiation antigen	M81750	1	0.01%	1	0.01%
837	peroxisomal acyl-CoA: dihydroxyacetonephosphate acyltransferase (DHAPAT)	AF043937	1	0.01%	1	0.01%
838	serologically defined colon cancer antigen 1 (SDCCAG1)	NM_004713.1	1	0.01%	1	0.01%
839	suppressor of G2 allele	NM_008704.1	1	0.01%	1	0.01%
840	methylene tetrahydrofolate dehydrogenase (NAD dependent), methen	NM_006636.1	1	0.01%	1	0.01%
841	aspartyl glucosaminidase (AGA)	X55330	1	0.01%	1	0.01%
842	osteoblast specific cysteine-rich protein, complete cds	AB008375	1	0.01%	1	0.01%
843	glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotr	NM_002080.1	1	0.01%	1	0.01%
844	proteinX0008 (AD013)	NM_013395.1	1	0.01%	1	0.01%
845	ubiquitin-activating enzyme E1C (homologous to yeast UBA3) (UBE1C)	gi4507764	1	0.01%	1	0.01%
846	CCAAT-box-binding transcription factor (CBF2)	NM_005760.1	1	0.01%	1	0.01%
847	c-Cbl-interacting protein (CIN85)	AF230904.1	1	0.01%	1	0.01%
848	GA-binding protein transcription factor, beta subunit 1 (53kd) (GABPB	NM_016654.1	1	0.01%	1	0.01%
849	thyroid receptor interactor (TRIP3)	L40410.1	1	0.01%	1	0.01%
850	ZNF01 and HUMORFKG1B genes, partial sequence	AF205588.1	1	0.01%	1	0.01%
851	endoplasmic reticulum lumenal Ca2 binding protein grp78	AF216292.1	1	0.01%	1	0.01%
852	leukophysin (LKP) = NM_001357.1 DEAD/H box polypeptide 9 (DDX9)	U03643.1	1	0.01%	1	0.01%
853	CGI-129 protein	AF151887.1	1	0.01%	1	0.01%
854	CGI-86 protein (LOC51635)	NM_016029.1	1	0.01%	1	0.01%
855	LIC-2 dynein light intermediate chain 53/55	U15138.1	1	0.01%	1	0.01%
856	protein 4.1-G, erythrocyte membrane protein (clone 24719)	AF054999	1	0.01%	1	0.01%
857	tropomodulin (TMOD)	M77016	1	0.01%	1	0.01%
858	TIP120 (=AB020636 KIAA0829)	D87671	1	0.01%	1	0.01%
859	orphan G protein-coupled receptor (RDC1)	U67784	1	0.01%	1	0.01%
860	mitogen-activated protein kinase 14 (MAPK14)	4503068	1	0.01%	1	0.01%
861	ralA binding protein 1 (RALBP1)	NM_006788.1	1	0.01%	1	0.01%
862	C-type lectin	BAA95671.1	1	0.01%	1	0.01%
863	non-histone chromosomal protein HMG-14	M21339.1	1	0.01%	1	0.01%
864	NCK adaptor protein 1 (NCK1)=X17576 melanoma mRNA for nck prote	NM_006153.1	1	0.01%	1	0.01%
865	cargo selection protein TIP47 (TIP47)(=PP17)	AF057140	1	0.01%	1	0.01%
866	CGI-43 protein	AF151801.1	1	0.01%	1	0.01%
867	DNA repair helicase (ERCC3)	M31899.1	1	0.01%	1	0.01%
868	UDP-GalNAc:polypeptide N-acetylglucosaminyltransferase (T1)	X85018	1	0.01%	1	0.01%
869	SMT3 (suppressor of mif two 3, yeast) homolog 1 (SMT3H1)	NM_006936.1	1	0.01%	1	0.01%
870	solute carrier family 20 (phosphate transporter), member 1 (SLC20A1)	7382462	1	0.01%	1	0.01%
871	glycogen phosphorylase	Y15233	1	0.01%	1	0.01%
872	ribonuclease L (2',5'-oligoadenylate synthetase-dependent) inhibitor	4506558	1	0.01%	1	0.01%
873	lymphocyte dihydropyrimidine dehydrogenase (DPYD)	U20938	1	0.01%	1	0.01%
874	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase) (UCHL	NM_006002.1	1	0.01%	1	0.01%
875	nuclear receptor coactivator (=TRBP)	AF245115	1	0.01%	1	0.01%
876	serine kinase SRPK2	U88666	1	0.01%	1	0.01%
877	acyl-coenzyme A:cholesterol acyltransferase (ORF)	L21934.2	1	0.01%	1	0.01%
878	NADP dependent cytoplasmic malic enzyme (=U43944)	X77244	1	0.01%	1	0.01%
879	leucine rich repeat (in FLII) interacting protein 1 (LRRFIP1) (=GCF2)	NM_004735.1	1	0.01%	1	0.01%
880	metalloprotease/disintegrin/cysteine-rich protein precursor (MDC9) (=D	U41766	1	0.01%	1	0.01%
881	host cell factor 2 (HCF-2)	NM_013320.1	1	0.01%	1	0.01%

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Figure 15 - Relative Est Frequency of Unique Known Genes Common to Mild and Severe cDNA Libraries - Page 18 of 19

882	X-ray repair complementing defective repair in Chinese hamster cells 4	gi4507944	1	0.01%	1	0.01%
883	cardiac myosin binding protein-C (ORF)	X84075	1	0.01%	1	0.01%
884	unc-50 related protein homologue	AF077038.1	1	0.01%	1	0.01%
885	activated in tumor suppression	AJ012502.1	1	0.01%	1	0.01%
886	cytokine-inducible SH2 protein 6 (CISH6) (=AB014571 KIAA0671)	AF073958.1	1	0.01%	1	0.01%
887	DAPIT protein	AJ271158	1	0.01%	1	0.01%
888	HepG2 3' region Mbol cDNA, clone hmd3c06m3	D17198.1	1	0.01%	1	0.01%
889	KIAA0008	D25304	1	0.01%	1	0.01%
890	KIAA0041	D26069	1	0.01%	1	0.01%
891	KIAA0095 gene	NM_014869.1	1	0.01%	1	0.01%
892	KIAA0227	D86980	1	0.01%	1	0.01%
893	KIAA0862=leucine-rich repeat protein SHOC-2 (SHOC-2)=AF054828	AB020689	1	0.01%	1	0.01%
894	KIAA0934 protein	AB023151.1	1	0.01%	1	0.01%
895	KIAA0997	NM_014950.1	1	0.01%	1	0.01%
896	KIAA1033	AB028956.1	1	0.01%	1	0.01%
897	KIAA1423	AB037844.1	1	0.01%	1	0.01%
898	La/SS-B protein	X68804	1	0.01%	1	0.01%
899	maternal-embryonic 3 (Mem3)	U47024	1	0.01%	1	0.01%
900	PB1	X90849	1	0.01%	1	0.01%
901	SCID complementing gene 2	D78188.1	1	0.01%	1	0.01%
902	TC1EL1 (t-complex-associated-testis-expressed 1-like 1)	D50663.1	1	0.01%	1	0.01%
903	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyl/galactosam	gi8393408	1	0.01%	1	0.01%
904	galactooxidase (GALC) gene	L38559	1	0.01%	1	0.01%
905	QUINONE OXIDOREDUCTASE (NADPH:QUINONE REDUCTASE) (Z	spQ08257	1	0.01%	1	0.01%
906	proline arginine-rich and leucine-rich repeat protein (PRELP) =U29089	NM_002725.1	1	0.01%	1	0.01%
907	selenoprotein T(LOC51714)	NM_016275.1	1	0.01%	1	0.01%
908	eukaryotic translation initiation factor 2 alpha kinase PEK	AF110146	1	0.01%	1	0.01%
909	EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5)	spP55010	1	0.01%	1	0.01%
910	translational inhibitor protein p14.5 (UK114) = X95384.1	NM_005836.1	1	0.01%	1	0.01%
911	translin associated protein X	X95073	1	0.01%	1	0.01%
912	ATP-dependent metalloprotease YME1L (contains Alu repeat)	AJ132637.1	1	0.01%	1	0.01%
913	proteasome subunit p42	D78275	1	0.01%	1	0.01%
914	sorting nexin 14 (SNX14)	AF121863.1	1	0.01%	1	0.01%
915	TIMP3 tissue inhibitor of metalloproteinases-3	X76227	1	0.01%	1	0.01%
916	ubiquitin conjugating enzyme, UbcH6	X92963	1	0.01%	1	0.01%
917	ubiquitin-conjugating enzyme E2D 3 (homologous to yeast UBC4/5) (U	NM_003340.1	1	0.01%	1	0.01%
918	ubiquitin-conjugating enzyme E2L 6 (UBE2L6) =AF061736 ubiquitin-co	NM_004223.1	1	0.01%	1	0.01%
919	WDR1 protein	AF020260	1	0.01%	1	0.01%
920	kaiso (ZNF-kaiso)	gi5803228	1	0.01%	1	0.01%
921	retinoblastoma-binding protein 2 (RBBP2)	NM_005056.1	1	0.01%	1	0.01%
922	Nuclear protein SA-2 (=STAG2)	Z75331.1	1	0.01%	1	0.01%
923	small nuclear ribonucleoprotein polypeptide B" (SNRBP2)	NM_003092.1	1	0.01%	1	0.01%
924	mitochondrial 12S and 16S rRNA	J01438	1	0.01%	1	0.01%
925	pre-mRNA cleavage factor Im (68kD) (CFIM) (=X67338)	5901927	1	0.01%	1	0.01%
926	male-specific lethal-3 (Drosophila)-like 1 (MSL3L1) (=DKFZp586J1822	NM_006800.1	1	0.01%	1	0.01%
927	nuclear protein stromal antigen 1 (SA-1)	NM_005862.1	1	0.01%	1	0.01%
928	coagulation factor V (proaccelerin, labile factor) (F5)	NM_000130.1	1	0.01%	1	0.01%
929	truncated SON protein (Son) (=AF161430.1 HSPC312)	AF193607.1	1	0.01%	1	0.01%
930	CGI-107 protein	AF151865.1	1	0.01%	1	0.01%
931	CGI-60 protein (LOC51626)	NM_016008.1	1	0.01%	1	0.01%
932	CGI-81 protein	AF151839.1	1	0.01%	1	0.01%
933	Norie disease protein (NDP)	X65882	1	0.01%	1	0.01%

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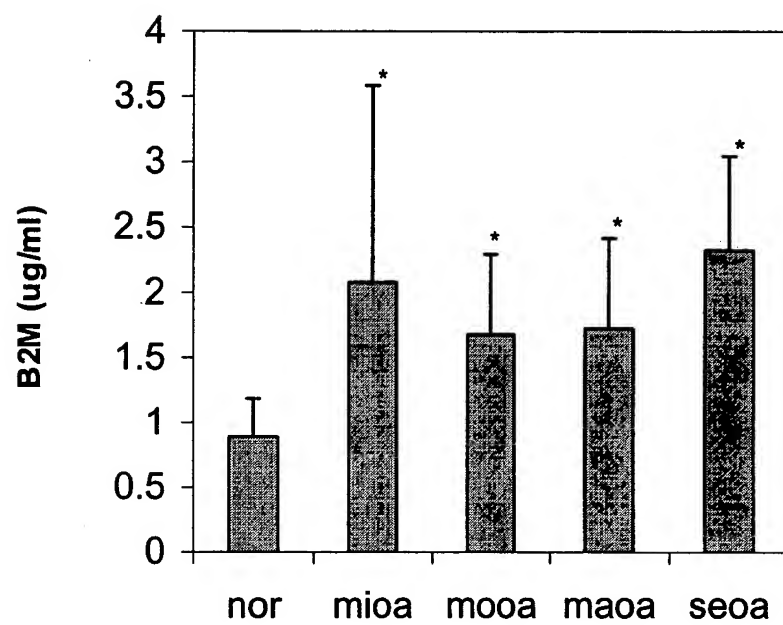
15

Figure 16 - Relative Est Frequency of Unique Known Genes Common to Mild and Severe cDNA Libraries - Page 19 of 19

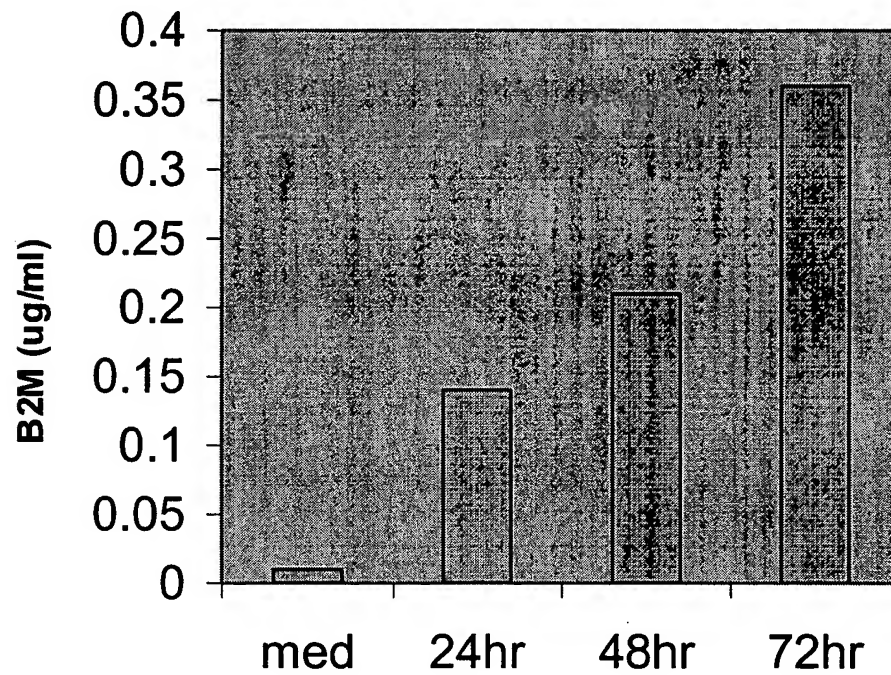
934	osteonidogen (=AJ223500 nidogen-2)	D86425	1	0.01%	1	0.01%
935	adapter protein CMS	AF146277.1	1	0.01%	1	0.01%
936	keratin 18 (K18)	M24842	1	0.01%	1	0.01%
937	myotubularin related protein 6	AF072928	1	0.01%	1	0.01%
938	nucleoporin p54	U63840	1	0.01%	1	0.01%
939	B219/OB receptor isoform HuB219.1	U52912	1	0.01%	1	0.01%
940	G protein-coupled receptor 68A (GPR68A) (=p40)	NM_006055.1	1	0.01%	1	0.01%
941	h-ryk	X69970.1	1	0.01%	1	0.01%
942	RYK tyrosine kinase	S59184.1	1	0.01%	1	0.01%
943	low-Mr GTP-binding protein (RAB32)	U59878	1	0.01%	1	0.01%
944	abundant in neuroepithelium area (BTG3) (=D64110 ANA)	gi5802989	1	0.01%	1	0.01%
945	glioblastoma amplified sequence (GBAS)	AF029786	1	0.01%	1	0.01%
946	macrophage-specific colony-stimulating factor (CSF-1)	M37435.1	1	0.01%	1	0.01%
947	monocyte chemotactic protein-3 (MCP-3)	X72308	1	0.01%	1	0.01%
948	ecotropic viral integration site 5 (EVI5)	NM_005865.1	1	0.01%	1	0.01%
949	potassium voltage-gated channel, delayed-rectifier, subfamily S, memb	NM_002252.1	1	0.01%	1	0.01%
950	Integrin, alpha V(vitronectin receptor, alpha polypeptide, antigen CD51)	NM_002210.1	1	0.01%	1	0.01%
951	chromodomain protein, Y chromosome-like (CDYL) =AF081259	NM_004824.1	1	0.01%	1	0.01%
952	GTP-binding protein RAB21 (RAB21) = KIAA0118	AF091035	1	0.01%	1	0.01%
953	neuronal apoptosis inhibitory protein	U19251	1	0.01%	1	0.01%
954	proto-oncogene (Wnt-5a)	L20681.1	1	0.01%	1	0.01%
955	tumor necrosis factor alpha-induced protein 6 (TNFAIP6)	NM_007115.1	1	0.01%	1	0.01%
956	solute carrier family 16 (monocarboxylic acid transporters), member 7	NM_004731.1	1	0.01%	1	0.01%
957	5' cap guanine-N-7 methyltransferase (RNMT)	AF067791.1	1	0.01%	1	0.01%

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Figure 17. B2M level in synovial fluid

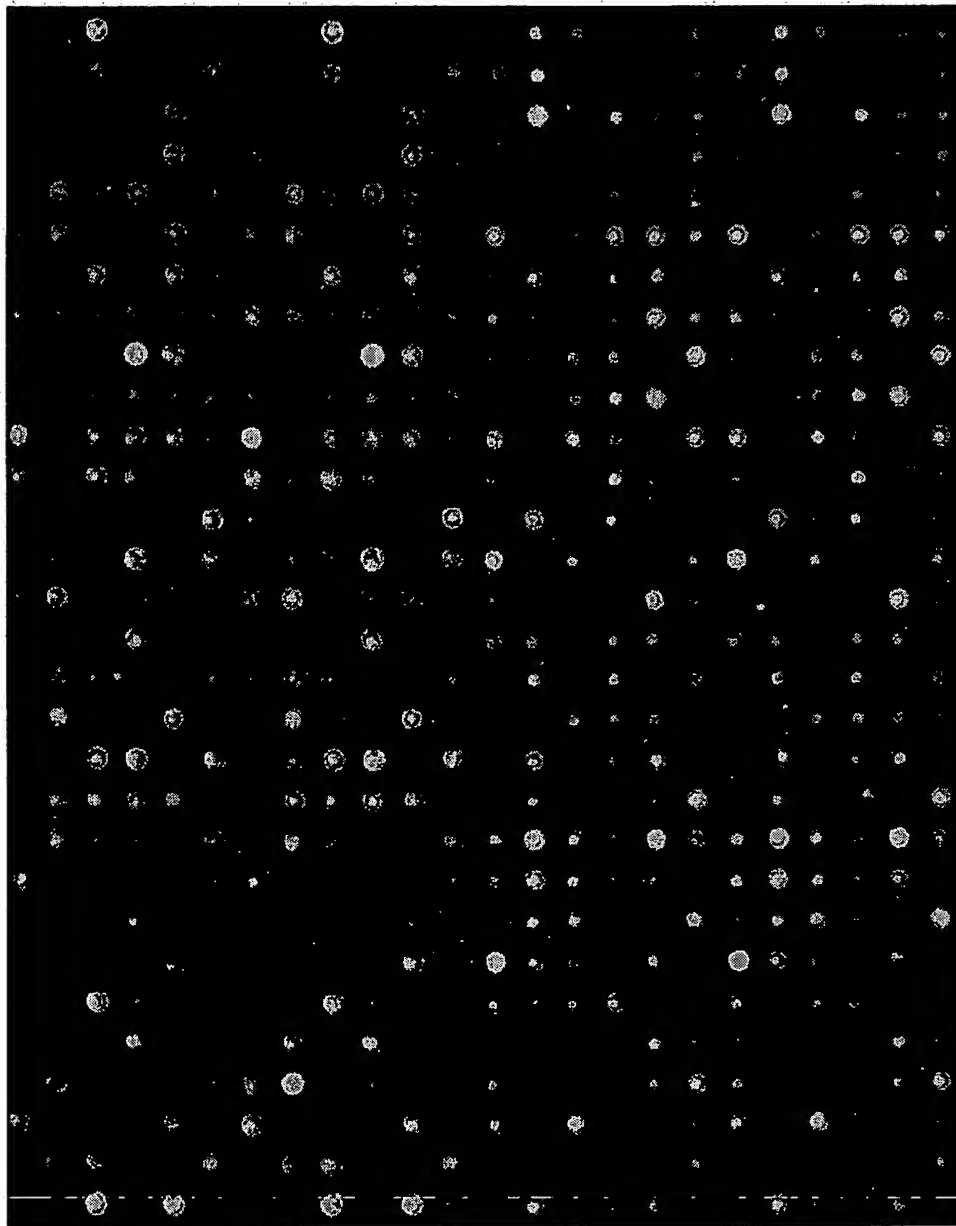


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Figure 18. B2M levels in severe OA cartilage cultured medium



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Figure 18. Differential gene expression of B2M treated chondrocytes detected by microarray.

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